

Run on:	March 12, 2005, 04:53:02 ; Search time 26.1438 Seconds (without alignments) 614.609 Million cell updates/sec		
Title:	US-10-049-182-4		
Perfect score:	870		
Sequence:	1 MHGTCFLWMPYLFVQ.....SRLQQSILQDMLWQLDLSPGC 167		
Scoring table:	BLOSUM62		
	Gapop 10.0 , Gapext 0.5		
Searched:	283416 seqs, 96216763 residues		
Total number of hits satisfying chosen parameters:	283416		
Minimum DB seq length:	0		
Maximum DB seq length:	200000000		
Post-processing: Minimum Match 0% Maximum Match 100%	Listing first 45 summaries		
Database :	PIR_79: 1: piri: 2: pir2: 3: pir3: 4: pir4:		
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	870	100.0 167 1 LTHU	leptin precursor - human
2	654.5	98.2 166 2 LTHU	leptin precursor - human
3	704	80.9 167 1 LTMS	leptin precursor - human
4	690	79.3 167 1 LTPT	leptin precursor - rat
5	690	79.3 167 2 A1055	probable soluble 1
6	84	9.7 639 2 A1055	hypothetical prote
7	81.5	9.4 226 2 AC1868	glutamate dehydro
8	81.5	9.4 1600 2 AB281	14-nm filament pro
9	81	9.3 462 2 JCS625	hypothetical prote
10	80.5	9.3 444 2 S54039	ATP-dependent RNA
11	79.5	9.1 296 2 D84511	hypothetical prote
12	79.5	9.1 696 2 S44912	hypothetical prote
13	79	9.1 409 2 B89954	hypothetical prote
14	79	9.1 829 2 T01362	probable myosin he
15	79	9.1 952 2 HB4583	hypothetical prote
16	79	9.1 1364 2 T40839	hypothetical prote
17	78	9.0 420 2 S75514	sensory transducti
18	78	9.0 421 2 AB2959	exopolysaccharide
19	78	9.0 423 2 D98324	exopolysaccharide
20	78	9.0 2513 2 G95336	hypothetical prote
21	77.5	8.9 460 2 F90097	hypothetical prote
22	77.5	8.9 574 1 B42374	phosphotransferase
23	77.5	8.9 1036 2 D70117	acrilavine resist
24	77	8.9 628 2 AB2889	hypothetical prote
25	76.5	8.8 173 2 S77486	ribosomal protein
26	76.5	8.8 362 2 AB3967	carbamoyl-phosphat
27	76.5	8.8 600 2 AB2233	lipoprotein inner
28	76.5	8.8 600 2 T47045	hypothetical prote
29	76.5	8.8 600 2 T17437	ybtp protein - Yer

RESULT 2



A; Reference number: 155622; MUID: 95386724; PMID: 7657834  
 A; Accession: 155622  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecule type: mRNA  
 A; Residues: 1-167 <PES>  
 A; Cross-references: GB:D45862; NID:91018990; PIDN:BAA08296.1; PID:91018991  
 C; Superfamily: leptin

Query Match 79.3%; Score 690; DB 2; Length 167;  
 Best Local Similarity 82.0%; Pred. No. 2.1e-14;  
 Matches 137; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MHWTGLLGFLLWWMPYLFFQAVPIQRVQDDDTKLIXTIVRINDISHTQSFKRTVGL 60  
 Db 1 MCWRPLCRLFLWNLWSYLSYQAVPIHVKQDDDTKLIXTIVRINDISHTQSARQTVGL 60

Qy 61 DFTPGHLHPITLTSKMDQTLAYQQIILTSMPSRNVIQISNDLENLRDILHVLAFSKSCLP 120  
 Db 61 DFTPGHLHPITLTSKMDQTLAYQQIILTSMPSRNVIQISNDLENLRDILHVLAFSKSCLP 120

Qy 121 WASGLETDLSGGVLEASGYSTEVVALLSRLQGSQSLQMLWQDLSPEC 167  
 Db 121 QTRGLQKPESDLGVLEASGYSTEVVALLSRLQGSQSLQMLWQDLSPEC 167

RESULT 6  
 AI0055 probable soluble lytic murein transglycosylase (EC 3.2.1.-) [imported] - Yersinia pestis  
 C; Species: Yersinia pestis  
 C; Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C; Accession: AI0055  
 R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature 413, 523-527, 2001  
 A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A; Reference number: AB0001; MUID:21470413; PMID:11586360  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-639 <PUR>  
 A; Cross-references: UNIPROT:Q8ZIP2; GB:AL590842; PIDN: CAC89308.1; PID:915978544; GSPDB:G  
 C; Genetics:  
 A; Gene: YPO0452  
 C; Superfamily: soluble lytic transglycosylase  
 C; Keywords: glycosidase; hydrolase

Query Match 9.7%; Score 84; DB 2; Length 639;  
 Best Local Similarity 21.7%; Pred. No. 14;  
 Matches 38; Conservative 22; Mismatches 41; Indels 74; Gaps 6;

Qy 12 LWPYLFFQAVPIQRVQDDDTKLIXTIVRINDISHTQSFKRTVGLDFTPGHLPLT 71  
 Db 59 LYPLEYRQL-----TDLQSVTQAQVKDFL-NRHPTLP 91

Qy 72 LSKMDQTLAVYQQIILTSMPSRNVIQISNDLENLRDILHVLAFSKSCLP-----120  
 Db 92 PAK-----SLPSRFV----NELARREDRIGLITFSPTAPKVAARCNYYAK 134

Qy 121 WASGLETDLSGGVLEASGYSTEVVALLSRLQGSQSLQD 156  
 Db 135 WATGEQSVAWEGASETILNGQSLPGSCDKEFSLPSVWQOQGHOTPLATLARMKLALKE 189

RESULT 7  
 AC1868 hypothetical protein a110492 [imported] - Nostoc sp. (strain PCC 7120)  
 C; Species: Nostoc sp. PCC 7120  
 A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C; Accession: AC1868  
 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, N.; Nakazaki, N.; Shimpoo, S.; Sugimoto, M.; Takazawa, M.; Tabata, S.

DNA Res. 8, 205-213, 2001  
 A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1887; MUID: 21595285; PMID: 11759810  
 A; Accession: AC1868  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-226 <PUR>  
 A; Cross-references: UNIPROT:Q8YZG8; GB:BA0000019; PIDN: BAB72450.1; PID:917129837; GSPDB:G  
 A; Experimental source: strain PCC 7120  
 A; Gene: a110492  
 C; Superfamily: Escherichia coli ygiH protein

Query Match 9.4%; Score 81.5; DB 2; Length 226;  
 Best Local Similarity 21.8%; Pred. No. 6.1;  
 Matches 41; Conservative 32; Mismatches 70; Indels 45; Gaps 6;

Qy 3 WGTLCGFELWLMMPYL-----YVQAVPIQRVQDDDTKLIXTIVRINDISHTQS 51  
 Db 4 WLSLGCAVVLVAVYLGSFPTGTYAVRQLKGDIREVGS-----TGATNVRLGK 55

Qy 52 SSQKQVGTGLDFTPGHLPLTISKMDQTLAYQQIILTSMPSRNVIQISNDLE-----NL 104  
 Db 56 GPGAFWVGLDCLKGV-----LAIALVYLYFFASQNLIPITVNIELWQPWLVTL 105

Qy 105 RDLLHVLAFSKSCHLFWASGLETLDSLGCVLEAS-----GYSTEVVALLSRLQGSQSLQD 156  
 Db 106 AGIAAIGHHSKSFIFGTGGKSVAATSGILLAMNNQVGLATFGVFAVVAISRV-SLSS 164

Qy 157 MLWQDLS 164  
 Db 165 IMGAATVS 172

RESULT 8  
 AB3281 glutamate dehydrogenase (EC 1.4.1.2) [imported] - Brucella melitensis (strain 16M)  
 C; Species: Brucella melitensis  
 C; Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 R; DelVecchio, V.G.; Kapatral, V.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
 A; Reference number: AD3282; PMID:11756688  
 A; Accession: AB3281  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-160 <PUR>  
 A; Cross-references: UNIPROT:Q8YJ55; GB:AE008917; PIDN: AAL51413.1; PID:917982118; GSPDB:G  
 A; Experimental source: strain 16M  
 A; Gene: BMB10231  
 A; Map position: I  
 C; Keywords: oxidoreductase

Query Match 9.4%; Score 81.5; DB 2; Length 1600;  
 Best Local Similarity 24.6%; Pred. No. 76;  
 Matches 32; Conservative 23; Mismatches 52; Indels 23; Gaps 5;

Qy 27 VQDDDTKLIXTIVRINDISHTQSFKRTGMDTQFLPILTSKMDTQFLAVYQQL 86  
 Db 97 VNDNNMFLLSIMGELND-HTSQI-----FMVWHPVLDISREKDELVILGEAS 143

Qy 87 TSMPSRNVIQISNDLENRLHVLAFSKSCLP WASGLETLDSLGCVLEASGYSTEVVA 146  
 Db 144 QLAPARGVERV-----LyQIHPALSKQAKADDTAGLKRV-LGQV-RSAVDWKPM 193

Qy 147 LSRLQGSQD 156  
 Db 194 LKRLDGAIID 203

RESULT 9  
 JC5625 14-nm filament protein/citrate synthase (EC 4.1.3.-) precursor - Tetrahymena thermophila  
 N;Alternate names: 49K filament-forming protein  
 C;Species: Tetrahymena thermophila  
 C;Accession: 14-Oct-1997 #sequence\_revision 07-Nov-1997 #text\_change 09-Jul-2004  
 R;Takeda, T.; Watanabe, Y.; Numata, O.  
 A;Title: Direct demonstration of the bifunctional property of tetrahymena 14-nm filament  
 A;Reference number: JC5625; MUID:97415775; PMID:9268867  
 A;Accession: JC5625  
 A;Molecule type: mRNA  
 A;Residues: 1-462 <TAK>  
 A;Cross-references: UNIPROT:P24118  
 R;Numata, O.; Takenaga, T.; Takagi, I.; Hirano, M.; Chiba, J.; Watanabe, Y.  
 Biochem. Biophys. Res. Commun. 174, 1028-1034, 1991  
 A;Title: Tetrahymena 14-nm filament-forming protein has citrate synthase activity.  
 A;Reference number: JN0130; MUID:91128358; PMID:1993043  
 A;Accession: JN0130  
 A;Molecule type: mRNA  
 A;Residues: 1-462 <NUM>  
 A;Cross-references: GB:D90117; NID:9217406; PIDN:BAA14145\_1; PID:gi1688046  
 A;Note: Part of this sequence, including the amino end of the mature protein, was confirmed by sequencing of the cDNA clone.  
 C;Comment: This protein is involved in oral morphogenesis preceding binary fission, and pronuclei. It also acts as a mitochondrial enzyme, citrate synthase.  
 C;Genetics:  
 A;Genetic code: SGCS  
 C;Superfamily: citrate synthase  
 C;Keywords: carbon-carbon lyase; cytoskeleton; mitochondrion; oxo-acid-lyase  
 F;1-21/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
 F;22-462/Product: 14-nm filament protein/citrate synthase #status experimental <MAT>

Query Match 9.3%; Score 81; DB 2; Length 462;  
 Best Local Similarity 26.4%; Pred. No. 17;  
 Matches 46; Conservative 26; Mismatches 54; Indels 48; Gaps 12;

Qy 14 PYLFYQAV----PIQKV--QDDDKTKLTKTIV---TRIND-----ISHTQSYSSKKV 57  
 Db 284 PYLSYSGAVNGLAGPHHGLANQEVLKWLQFIBERGKTVSDKDLEDYDVRV--LSSGRV 341  
 Db 288 PYGLW----DFIPGLHPLTLISKM---DQTLLAVYQQQLTSMPSRNVII-QISNDLENIR 105  
 Qy 58 TGL----DFIPGLHPLTLISKM---DQTLLAVYQQQLTSMPSRNVII-QISNDLENIR 105  
 Db 342 PGYGHAVLRDQDPRFHQVDFSKFLKDQMIKLHQCAADPKKLTKTYYKIANPYNP- 400  
 Qy 106 DLLHVAIATFSKCHLPLWAGLTLTLDLGGVLEASGSTEVALSRLQGSQDMWL 159  
 Db 401 -----DCH----SGV-LLYSLIG--LTYEQYTTVFAVSRALGCMANLW 437

RESULT 10  
 hypothetical protein YDR055W - yeast (Saccharomyces cerevisiae)  
 N;Alternate names: hypothetical protein D4214; hypothetical protein YBRB444; hypothetical protein YDR055W  
 C;Species: Saccharomyces cerevisiae  
 C;Accession: 08-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
 R;Hunt, S.; Bowman, S.; Harris, D.  
 A;Reference number: S54031  
 A;Accession: S54031  
 A;Molecule type: DNA  
 A;Residues: 1-444 <HUN>  
 A;Cross-references: UNIPROT:Q12355; EMBL:Z49209; NID:9798897; PIDN:CAA89084\_1; PID:gi79898  
 R;Brandt, P.; Otto, B.; Ramlow, S.; Bloecker, H.  
 Submitted to the EMBL Data Library, January 1995  
 A;Reference number: S58835  
 A;Accession: S58835  
 A;Molecule type: DNA  
 A;Residues: 1-444 <DNA>  
 A;Cross-references: EMBL:X84162; NID:9706817; PIDN:CAA58971\_1; PID:gi7068821  
 R;Brandt, P.; Ramlow, S.; Otto, B.; Bloecker, H.  
 Yeast 12, 85-90, 1996

RESULT 11  
 D88511 ATP-dependent RNA helicase homolog [imported] - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
 C;Accession: D88511  
 R;Anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology  
 A;Reference number: A75000; MUID:99059613; PMID:9851916  
 A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/ and  
 A;Accession: D88511  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-296 <STO>  
 A;Cross-references: GB chr III; PIDN:AAA28179\_1; PID:gi289738; GSPDB:GN00021  
 A;Note: homology with ATP-dependent RNA helicase; putative  
 C;Genetics:  
 A;Map position: 3

Query Match 9.1%; Score 79.5; DB 2; Length 296;  
 Best Local Similarity 29.2%; Pred. No. 13;  
 Matches 33; Conservative 12; Mismatches 31; Indels 37; Gaps 6;

Qy 10 LWLW----PYLFYQQVPIQVKQDFTKPLKTKLTKTIVRINDSIT-----QSVSQKV 58  
 Db 33 LHLWNLFKPBLSATAVS-----VQDTTSQPOVDHYSGRLAPSSSTSHRLVVT 81  
 Qy 59 GLDPFPGLHPLTLISKMQLTAYQQQLTSMPSRNVIIQSNDLENRLDILHVL 111  
 Db 82 D----PKFHP-----LAVYQQTTRNKFNRTLIFV-NEVSSSNRLAHVL 119

RESULT 12	Qy 19 VQAVPIQKVQDDDTKVLKTIKIV-----TRINDISHTQSVSQKQVTKGLDFIPGSIH--- 67
S44912	Db 101 INGVITALNTIDTEFLIKTVKLLENNYGGINLEDISAPRCFEIERLKKETNIPFHDDQ 160
hypothetical protein ZK86.2 - Caenorhabditis elegans	N; Contains: hypothetical protein Z97.2
C; Species: Caenorhabditis elegans	68 ---PLTLSKMDQTTAVYQOILTSMPRSRNVIQISNDLENLRLHLH----VLAFSKSCHL 119
C; Date: 20-Feb-1995 #text_change 09-Jul-2004	R; Lin, X.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uti, Y.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
C; Accession: S44912; S44884	Lancet, D.; 125-1240, 2001
R; Du, Z.	A; Title: Whole Genome sequencing of meticillin-resistant Staphylococcus aureus.
Submitted to the EMBL Data Library, June 1993	A; Reference number: A89758; PMID:21311952; PMID:11418146
A; Accession: S44909	A; Molecule type: DNA
A; Residues: 1-696 <DUZ>	A; Residues: 1-409 <KDR>
A; Cross-references: UNIPROT:P34668; EMBL:L17337; NID:9304345; PIDN:AAA28223.1; PID:93043	A; Cross-references: UNIPROT:P34668; EMBL:L17337; NID:9304345; PIDN:AAA28223.1; PID:93043
R; Du, Z.	R; Du, Z.
Submitted to the EMBL Data Library, May 1993	Submitted to the EMBL Data Library, May 1993
A; Description: Sequence of the C. elegans cosmid ZC97.	A; Description: Sequence of the C. elegans cosmid ZC97.
A; Reference number: S44615	A; Reference number: S44615
A; Accession: S44884	A; Accession: S44884
A; Molecule type: DNA	A; Molecule type: DNA
A; Residues: 1401-696 DDBJ	A; Residues: 1401-696 DDBJ
A; Cross-references: EMBL:L14714; NID:9289737; PIDN:AAA28179.1; PID:9289738	A; Cross-references: EMBL:L14714; NID:9289737; PIDN:AAA28179.1; PID:9289738
A; Experimental source: cosmid ZC97	A; Experimental source: cosmid ZC97
A; Note: designated as ZC97.2 protein	A; Note: designated as ZC97.2 protein
A; Genetics:	A; Genetics:
A; Introns: 15/1; 89/3; 102/3; 120/3; 145/3; 194/2; 312/2; 453/3; 643/2	A; Introns: 15/1; 89/3; 102/3; 120/3; 145/3; 194/2; 312/2; 453/3; 643/2
C; Keywords: AdP; nucleotide binding; P-loop	C; Keywords: AdP; nucleotide binding; P-loop
F; 266-272/Region: nucleotide-binding motif A (P-loop)	F; 266-272/Region: nucleotide-binding motif A (P-loop)
F; 313-378/Region: nucleotide-binding motif B	F; 313-378/Region: nucleotide-binding motif B
F; 377-380/Region: DEAD motif	F; 377-380/Region: DEAD motif
F; 401-696/Product: hypothetical protein ZC97.2 #status predicted <ZCP>	F; 401-696/Product: hypothetical protein ZC97.2 #status predicted <ZCP>
Query Match 9.1%; Score 79.5; DB 2; Length 696;	Query Match 9.1%; Score 79.5; DB 2; Length 696;
Best Local Similarity 29.2%; Pred. No. 39; Matches 33; Conservative 12; Mismatches 31; Indels 37; Gaps 6;	Best Local Similarity 29.2%; Pred. No. 39; Matches 33; Conservative 12; Mismatches 31; Indels 37; Gaps 6;
Qy 10 LWLW---PLTFVVAQVPIQKVQDDDTKVLKTIKIVTRINDISHT-----QSVSRSRKVT 58	Qy 10 LWLW---PLTFVVAQVPIQKVQDDDTKVLKTIKIVTRINDISHT-----QSVSRSRKVT 58
Db 433 LHWNLKPRLPSAVS-----VKDITSGIPQDVHSGRLLAQLSSISHRLVVT 481	Db 433 LHWNLKPRLPSAVS-----VKDITSGIPQDVHSGRLLAQLSSISHRLVVT 481
Qy 59 GLDFIFGLHPILTLSKMDQTTAVYQOILTSMPRSRNVIQISNDLENLRLHLH 111	Qy 59 GLDFIFGLHPILTLSKMDQTTAVYQOILTSMPRSRNVIQISNDLENLRLHLH 111
Db 482 D----PKFHP-----DAVQQTTRANKPNRFLIFT-NEVSSSNRILAHVL 519	Db 482 D----PKFHP-----DAVQQTTRANKPNRFLIFT-NEVSSSNRILAHVL 519
Query Match 9.1%; Score 79; DB 2; Length 829;	Query Match 9.1%; Score 79; DB 2; Length 829;
Best Local Similarity 21.5%; Pred. No. 54; Matches 34; Conservative 27; Mismatches 45; Indels 52; Gaps 6;	Best Local Similarity 21.5%; Pred. No. 54; Matches 34; Conservative 27; Mismatches 45; Indels 52; Gaps 6;
Qy 24 IQKVQDDDTKVLKTIKIVTRINDISHTQSVSRSRKVTQDFPGLHPILTLSKMDQTKVY- 82	Qy 24 IQKVQDDDTKVLKTIKIVTRINDISHTQSVSRSRKVTQDFPGLHPILTLSKMDQTKVY- 82
Db 57 ISRVVSD--SITRGWTAIES-----DIAEKIAQKD-----LELSKIRETLYH 99	Db 57 ISRVVSD--SITRGWTAIES-----DIAEKIAQKD-----LELSKIRETLYH 99
Qy 83 -----QQLTSMPSRNVIQISNDLENLRLHLH----- 120	Qy 83 -----QQLTSMPSRNVIQISNDLENLRLHLH----- 120
Db 100 VGSBNEESSESSLINDELQIQQSSSSKKRQLMLVEELTNRKYIHN----- 150	Db 100 VGSBNEESSESSLINDELQIQQSSSSKKRQLMLVEELTNRKYIHN----- 150
Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRLQGSQCDML 158	Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRLQGSQCDML 158
Db 151 -GSGATVDDSLG--LDSSPHETRSTKVDRMLDSLSKIL 185	Db 151 -GSGATVDDSLG--LDSSPHETRSTKVDRMLDSLSKIL 185
RESULT 13	RESULT 15
B89954	H84583
hypothetical protein SA1524 [imported] - Staphylococcus aureus (strain N315)	hypothetical protein At2920010 [imported] - Arabidopsis thaliana
C; Species: Staphylococcus aureus	C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004	C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C; Accession: B89954	C; Accession: H84583
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uti, Y.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.	R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J;
A; Title: Whole Genome sequencing of meticillin-resistant Staphylococcus aureus.	A; Title: Whole Genome sequencing of meticillin-resistant Staphylococcus aureus.
A; Reference number: A89758; PMID:21311952; PMID:11418146	A; Reference number: A89758; PMID:21311952; PMID:11418146
A; Status: preliminary	A; Status: preliminary
A; Molecule type: DNA	A; Molecule type: DNA
A; Residues: 1-409 <KDR>	A; Residues: 1-409 <KDR>
A; Cross-references: UNIPROT:Q99TGI; GB:BA000018; PIDN:G13701497; PIDN:BAB42791.1; GSPDB:G	A; Cross-references: UNIPROT:Q99TGI; GB:BA000018; PIDN:G13701497; PIDN:BAB42791.1; GSPDB:G
C; Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)	C; Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)
A; Gene: SA1524	A; Gene: SA1524
A; Experimental source: strain N315	A; Experimental source: strain N315

Nature 402, 761-768, 1999  
A; Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A; Reference number: A84420; PMID:20083487; PMCID:10617197  
A; Accession: H84583  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-952 <STO>  
A; Cross-references: UNIPROT:Q9SL80; GB:AE002093; NID:94580471; PIDN:AADD4395.1; GS-C; Genetics:  
A; Gene: At2g20010  
A; Map position: 2

Search completed: March 12, 2005, 05:04:35  
Job time : 30.1438 secs

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4 protein - protein search, using SW model	
run on:	March 12, 2005, 04:44:03 ; Search time 124.85 Seconds (without alignments) 517.333 Million cell updates/sec
title:	US-10-049-182-4
effect score:	870
Sequence:	1 MHKGTLICGFLWLPYLFFVQ. .... .SRLQGSLOQDMLWQDLDLSPGC 167
scoring table:	BLOSUM62
Gappen:	10.0 , Gapext 0.5
searched:	2105692 seqs, 386760381 residues

ALIGNMENTS							
<b>RESULT 1</b>							
AAW03694 standard; protein: 167 AA.							
ID AAW03694;							
XX XX AC DT 15-JUL-1997 (first entry)							
Human obese (ob) protein.							
XX KW Human; obese; ob; body; weight; modulation; defect; mutation; prevention; interference; production; function; treatment; control; obesity; disease; reduction; food intake; gain; mammal; type II; diabetes; mellitus; hypertension; hyperlipidaemia; identification; receptor.							
DE							
XX Homo sapiens.							
OS XX							
FH Key Location/Qualifiers							
FT Peptide 1..21 /label= sig_peptide							
FT Peptide 22..167 /label= mat_peptide							
FT FT							
XX XX							
EP741187-A2.							
XX XX							
06-NOV-1996.							
XX XX							
PF 24-APR-1996; 96EP-00106408.							
XX XX							
PR 05-MAY-1995; 95US-00435777.							
PR 07-JUN-1995; 95US-00484629.							
XX XX							
PA (HOFF ) HOPPEMANN LA ROCHE & CO AG F.							
XX XX							
PI Campfield A, Devos R, Guisez Y;							
XX XX							
DR WPI: 1996-487390/49.							
DR N-PSDB; AAT42168.							
XX XX							
PT New isolated human and murine obese proteins - and related DNA, used for the treatment, prevention and control of obesity and associated diseases.							
XX XX							
PT The present sequence is the human obese (ob) protein, a body weight modulator, which can be administered to patients suffering from ob gene defects or mutations which prevent or interfere with its production and/or function. The Ob protein can be used to treat, prevent or control							
CC CC CC CC							
The present sequence is the human obese (ob) protein, a body weight modulator, which can be administered to patients suffering from ob gene defects or mutations which prevent or interfere with its production and/or function. The Ob protein can be used to treat, prevent or control							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
%							
Result No.	Score		Match Length	DB ID	Description		
1	870	100.0	167	2	AAW03694 Human obe		
2	870	100.0	167	2	AAR99473 Human ob		
3	870	100.0	167	2	AAR92720 Obesity P		
4	870	100.0	167	2	AAW34060 Human obe		
5	870	100.0	167	2	AAW7442 Human Lep		
6	870	100.0	167	3	AAV82110 Human obe		
7	870	100.0	167	3	AAB28448 Human OB		
8	870	100.0	167	3	AAY84190 Amino aci		
9	870	100.0	167	3	AAV80259 Human obe		
10	870	100.0	167	3	AAY87726 Murine OB		
11	870	100.0	167	3	AAB28467 Human OB		
12	870	100.0	167	3	AAV59914 Human Lep		
13	870	100.0	167	4	AAB72927 Human Lep		
14	870	100.0	167	4	AAC10338 Human Lep		
15	870	100.0	167	4	AAU02890 Human Ob		
16	870	100.0	167	4	AAB70128 Human Lep		
17	870	100.0	167	5	ABG74164 Human obe		
18	870	100.0	167	6	ABU84116 Human Ob		
19	870	100.0	167	6	ABU4561 Human obe		
20	870	100.0	167	7	ADBS6246 Human Pro		
21	870	100.0	167	7	ADF15260 Human Alb		
22	870	100.0	167	7	ADF15253 Human alb		
23	870	100.0	167	7	ADF15257 Human alb		
24	870	100.0	167	7	ADF15259 Human alb		
25	870	100.0	167	7	ADH21374 Human lep		

Sequence 167 AA:							
	Query Match	Score	DB	Length			
C	Best Local Similarity	100.0%	Pred. No.	4.8e-95			
C	Matches	167	Conservative	0	Mismatches	0	
C					Indels	0	
C					Gaps	0	
C							
C	1 MHWGTCGELMIPWPLFYVQAVPIQKQVQDDDKTLIKIVTRINDI	100.0%	I	100.0%	Score	870;	
C	1 MHWGTCGELMIPWPLFYVQAVPIQKQVQDDDKTLIKIVTRINDI	100.0%	I	100.0%	DB	2;	
C					Length	167;	
C							
C	61 DFIPGHPILTLSKMDQTLAYQQILITSMPSRNVIQISNDLLENL	100.0%	I	100.0%	Pred. No.	4.8e-95	
C	61 DFIPGHPILTLSKMDQTLAYQQILITSMPSRNVIQISNDLLENL	100.0%	I	100.0%	Mismatches	0	
C					Indels	0	
C					Gaps	0	
C							
X	121 WASGLLETLDLSGGVLPLASGYSTEVVALSRLGQSIIQMLIWOLDLSPGC	100.0%	I	100.0%	Score	870;	
X	121 WASGLLETLDLSGGVLPLASGYSTEVVALSRLGQSIIQMLIWOLDLSPGC	100.0%	I	100.0%	DB	2;	
X					Length	167;	
X							
b	Y	1 MHWGTCGELMIPWPLFYVQAVPIQKQVQDDDKTLIKIVTRINDI	100.0%	I	100.0%	Pred. No.	4.8e-95
b	Y	1 MHWGTCGELMIPWPLFYVQAVPIQKQVQDDDKTLIKIVTRINDI	100.0%	I	100.0%	Mismatches	0
b	b				Indels	0	
b	b				Gaps	0	
b	b						
b	Y	61 DFIPGHPILTLSKMDQTLAYQQILITSMPSRNVIQISNDLLENL	100.0%	I	100.0%	Score	870;
b	Y	61 DFIPGHPILTLSKMDQTLAYQQILITSMPSRNVIQISNDLLENL	100.0%	I	100.0%	DB	2;
b	b				Length	167;	
b	b						
b	121 WASGLLETLDLSGGVLPLASGYSTEVVALSRLGQSIIQMLIWOLDLSPGC	100.0%	I	100.0%	Pred. No.	4.8e-95	
b	121 WASGLLETLDLSGGVLPLASGYSTEVVALSRLGQSIIQMLIWOLDLSPGC	100.0%	I	100.0%	Mismatches	0	
b	b				Indels	0	
b	b				Gaps	0	
b	b						

RESULT 2	AAR99473	standard; protein; 167 AA.	XX	RESULT 3	AAR92720	standard; protein; 167 AA.	XX
D	AA999473		ID	AAR92720			
X	AAR99473;		XX				
C			AC				
X							
X	22-OCT-1996	(first entry)	XX				
X			DT	12-SEP-1996	(first entry)		
E	Human ob protein.		XX				
X			DE	Obesity protein.			
X	Obesity; ob gene; ob protein; appetite suppression factor.		XX				
S	Homo sapiens.		KW	Obesity; mouse; Oba; leptin; hormone; body weight regulation; diabetes;			
S			KW	food intake; energy expenditure; high blood pressure; cholesterol; human			
X			KW	gene therapy; antibody; cancer; robe beef; Foie gras; immunoassay.			
H			XX				
H	Key Peptide		OS	Homo sapiens.			
T	Protein		XX				
T			FH				
T			Peptide	Key			
K	WO9622308-A2.		FT	Peptide	1..21		
K			FT		/note= "signal peptide"		
K			FT	Protein	22..167		
K			FT		/note= "obesity protein"		
O	25-JUL-1996.		XX				
X			PN	GB229238-A.			
X			XX				
F	22-JAN-1996;	96WO-US001471.	PD	21-FEB-1996.			
F			XX				
R			PF	17-AUG-1995;	95GB-00016947.		
R	20-JAN-1995;	95US-00377068.	XX				
R	10-APR-1995;	95US-00419214.	PF				
R	07-JUN-1995;	95US-00486450.	XX				
R	07-JUN-1995;	95US-00486459.	PR	17-AUG-1994;	94US-0092345.		
R	07-JUN-1995;	95US-00487111.	PR	30-NOV-1994;	94US-00347563.		
R	04-OCT-1995;	95US-00540242.	PR	10-MAY-1995;	95US-00438431.		
R			PR	07-JUN-1995;	95US-00483211.		
A	(ZYMO ) ZYMOGENETICS INC.		XX				
A	(UNIW ) UNIV WASHINGTON.		PA	(UTRQ ) UNIV ROCKEFELLER.			
A	Weigle DS, Kuijper JL, Bukowski TR;		XX				
A			PI	Friedman JM, Zhang Y,			
A			PI	Proenca R,			
A			Burley SK;	Maffei M,			
A			XX	Halaas JL,			
A			DR	Gajiwala K;			
A			DR				
A			WPI; 1996-099009/11.				
A			N-PSDB; AAT16373.				
A	Identifying factors that regulate appetite, e.g. for treatment of obesity		XX	Obesity polypeptide(s) able to modulate body wt. - useful for e.g.			
A	- by administering a test sample to a mammal and determining decrease in		PT	reducing wt. in treatment of diabetes, high blood pressure and high			
A	food consumption.		PT	cholesterol and for cosmetic reasons.			
A			XX				
S	Claim 6; Page 76; 90pp; English.						

PS Claim 2; p171-172; 304pp; English.

XX This sequence represents the human obesity polypeptide (OBP). OBP (also known as leptin) is a hormone involved in the regulation of body weight. CC This sequence has effects on both food intake and energy expenditure. OBP CC and its analogues are useful for modifying body weight (optionally combined with known medicaments), for treating diabetes, high blood CC pressure or high cholesterol. The DNA encoding this sequence (and CC sequences complementary to it) can be used in gene therapy for modifying CC body weight. This protein can be used for reducing weight for health or CC cosmetic reasons in obese humans, or to produce leaner food animals. CC Antagonists of OBP (including antibodies) are useful for increasing body CC weight, e.g. for treating weight loss associated with cancer, or for CC cosmetic reasons in humans, or for production of Kobe beef or Foie gras CC in domestic animals. OBP antibodies (Ab) can also be used in diagnostic CC immunoassays for the presence of OBP. The formation of Ab-OBP complexes CC enables in vitro evaluation of levels of OBP in a sample, especially to CC detect diseases associated with elevated or decreased levels, and to CC monitor treatment of these diseases

XX Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;

Best Local Similarity 100.0%; Pred. No. 4.8e-85; Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ

1 MHWGTLCGFMLWPYLFFYQAVPIQKYYQDDTTKLIKTVTRINDISHTQSVSSTKQVTL 60  
Db 1 MHWGTLCGFMLWPYLFFYQAVPIQKYYQDDTTKLIKTVTRINDISHTQSVSSTKQVTL 60Qy 61 DFIPGLHPITLTKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLYLAFSKSCHLP 120  
Db 61 DFIPGLHPITLTKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLYLAFSKSCHLP 120Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRQLGSQDMLWQDLSPGC 167  
Db 121 WASGLETLDSLGGVLEASGYSTEVALSRQLGSQDMLWQDLSPGC 167RESULT 4  
AAW34060  
ID AAW34060 standard; protein; 167 AA.  
AC AAW34060;  
XX DT 24-APR-1998 (first entry)  
XX DE Human obese (ob) protein.  
XX KW Obese protein; ob protein; osteogenic cell; bone-forming activity;  
KW migration; bone-forming cell; marrow mesenchymal cell; bone repair;  
KW bone healing; bone loss.  
XX OS Homo sapiens.  
FH Key Peptide  
FT Location/Qualifiers  
FT 1..21  
FT /note= "signal peptide"  
XX PN WO9739767-A1.  
XX PD 30-OCT-1997.  
XX PP 18-APR-1997; 97WO-US006892.  
XX PR 19-APR-1996; 96US-0015647P.  
XX PA (ZYMO ) ZYMOGENETICS INC.  
PA (UNIV ) UNIV WASHINGTON.  
XX PI Durnam DM, Kuijper JL, Weigle DS, Liu CC;  
XX DR WPI; 1997-535577/49.

N-PSDB; AAT93021.

DR XX Use of obese protein for inducing bone formation - particularly for PT treating osteoporosis, repairing fractures, dental defects or PT resectioning due to oncogenesis.

XX Disclosure; Page 32; 42pp; English.

XX The present sequence represents a human obese (ob) protein. DNA sequence CC was isolated from an adipose tissue cDNA library using a probe derived CC from the mouse obese gene. ob proteins can produce a dramatic increase in CC osteogenic cells or their bone-forming activity. They can enhance CC recruitment or migration of bone-forming cells to the proper bone-forming CC tissues and tissue sites. The ob protein was used in the method of the CC invention, which involves the stimulation of cell population containing CC marrow mesenchymal cells. The method comprises exposing the cell CC population to an ob protein for expansion of osteogenic cells, a biological fluid obtained from an ob protein-treated mammal, or a culture CC medium that has been conditioned by growth of endocrine or CNS cells or CC tissue exposed to ob protein. The method can be used in a mammal for CC promoting bone repair or bone healing, stimulating bone ingrowth into a CC prosthetic device or dental implant that has been inserted into a mammal, CC for treating bone loss, for increasing bone length, for stimulating active bone growth, or for inducing bone formation

SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 4.8e-85;  
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 1 MHWGTLCGFMLWPYLFFYQAVPIQKYYQDDTTKLIKTVTRINDISHTQSVSSTKQVTL 60  
Db 1 MHWGTLCGFMLWPYLFFYQAVPIQKYYQDDTTKLIKTVTRINDISHTQSVSSTKQVTL 60Qy 61 DFIPGLHPITLTKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLYLAFSKSCHLP 120  
Db 61 DFIPGLHPITLTKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLYLAFSKSCHLP 120Qy 61 DFIPGLHPITLTKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLYLAFSKSCHLP 120  
Db 61 DFIPGLHPITLTKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLYLAFSKSCHLP 120Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRQLGSQDMLWQDLSPGC 167  
Db 121 WASGLETLDSLGGVLEASGYSTEVALSRQLGSQDMLWQDLSPGC 167

RESULT 5

AAW57442  
ID AAW57442 standard; peptide; 167 AA.  
XX AC AAW57442;  
XX DT 10-AUG-1998 (first entry)  
DE Human leptin sequence.  
XX KW Leptin; murine; antagonist; treatment; type II diabetes; insulin; human.  
XX OS Homo sapiens.  
XX FH Key  
FT Disulfide-bond  
FT Location/Qualifiers  
XX 7..167  
FT /note= "disulphide bridge"  
XX PN WO9812224-A1.

XX XX 26-MAR-1998.  
XX XX 97WO-EP005035.  
XX XX 15-SEP-1997;  
XX XX 96DE-01038487.  
XX XX (FARH ) HOECHST AG.  
XX XX Ertel J, Preibisch G, Mueller G;

XX WPI; 1998-217209/19.  
 XX Use of leptin antagonists - for restoring or amplifying the physiological effect of insulin in the treatment of Type II diabetes.  
 XX Disclosure; Page 19; 30pp; English.  
 XX This is a human leptin protein sequence which is highly homologous to the murine leptin sequence. The carboxyl-terminal fragment of the murine leptin can act as a leptin antagonist. This can be used in a pharmaceutical composition which comprises the murine leptin fragment which is therapeutically beneficial for the treatment of Type II diabetes. The leptin antagonists include Peptides derived from Leptin fragments and may be obtained by chemically or enzymatically cleaving intact leptin or by recombinant expression using microorganisms. This fragment can be prepared by digestion of leptin with lysyl endopeptidase. The leptin antagonists can restore or amplify the physiological effect of insulin by inhibiting leptin-induced insulin resistance

Sequence 167 AA;  
 Query Match 100.0%; Score 870; DB 2; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;  
 Matches 167; Conservative 0; N mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MHWGLICGFLMLWPVLFYQAVPIQKVQDDTKLIRKTIIVRINDISHTQS VSSSQKVTL 60  
 Db 1 MHWGLICGFLMLWPVLFYQAVPIQKVQDDTKLIRKTIIVRINDISHTQS VSSSQKVTL 60  
 Qy 61 DFIPGLHPILTSKMDQTAVQQLTSMPSRNTVQISNDLENRLDHLVLA FSKSCHLP 120  
 Db 61 DFIPGLHPILTSKMDQTAVQQLTSMPSRNTVQISNDLENRLDHLVLA FSKSCHLP 120  
 Qy 121 WASGLETLDSLGTVLEASGYSTEVALSRQLGSLSQDMWQLDLSPGC 167  
 Db 121 WASGLETLDSLGTVLEASGYSTEVALSRQLGSLSQDMWQLDLSPGC 167

RESULT 6  
 AAY82110 Human obese protein SEQ ID NO:5.  
 ID AAY82110 standard; protein; 167 AA.  
 AC AAY82110;  
 XX 05-JUN-2000 (first entry)  
 DE Human obese protein  
 KW Ob gene; ob protein; obesity; body weight; polyethylene; obese protein; polypropylene; protein conjugate; anorectic.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 XX US625324-A.  
 PD 15-FEB-2000.  
 XX 15-MAY-1996; 96US-00648262.  
 XX 15-MAY-1996; 96US-00648262.  
 XX (HOFF ) HOFFMANN LA ROCHE INC.

XX Ballon PS, Devos R, Campfield A, Guisez Y;  
 XX WPI; 2000-222636/19.  
 DR N-PDB; AAC62566.  
 XX PR Nucleic acid primers and probes useful for detecting mutations in mammalian OB gene associated with regulation of body weight and adiposity.  
 PT XX WPI; 2000-601556/57.  
 DR N-PDB; AAC62566.  
 XX PR Nucleic acid primers and probes useful for detecting mutations in mammalian OB gene associated with regulation of body weight and adiposity.  
 PT XX WPI; Fig 3; 153pp; English.

XX The present sequence is encoded by a nucleotide sequence used in an invention relating to the control of body weight of animals including humans. Nucleic acids of at least 10 nucleotides which are hybridizable to a non-coding region of an OB nucleic acid have been created. The OB gene plays a critical role in the regulation of body weight and adiposity. The nucleic acids may be used as probes or as primers for PCR. They are useful for evaluating the presence of mutations in the human OB gene or for evaluating the level of expression of OB mRNA. Defects

PS Disclosure; Col 35-36; 26pp; English.

XX The present invention describes a composition comprising one or more polyethylene and polypropylene human obese protein conjugates (I). The composition has anorectic activity. The conjugates are used for the treatment, prevention and control of obesity and associated conditions in humans and animals. The present sequence represents the human obese protein

XX Sequence 167 AA;  
 Query Match 100.0%; Score 870; DB 3; Length 167;

Best Local Similarity 100.0%; Pred. No. 4.8e-85;  
 Matches 167; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGLICGFLMLWPVLFYQAVPIQKVQDDTKLIRKTIIVRINDISHTQS VSSSQKVTL 60

Db 1 MHWGLICGFLMLWPVLFYQAVPIQKVQDDTKLIRKTIIVRINDISHTQS VSSSQKVTL 60

Qy 61 DFIPGLHPILTSKMDQTAVQQLTSMPSRNTVQISNDLENRLDHLVLA FSKSCHLP 120

Db 61 DFIPGLHPILTSKMDQTAVQQLTSMPSRNTVQISNDLENRLDHLVLA FSKSCHLP 120

Qy 121 WASGLETLDSLGTVLEASGYSTEVALSRQLGSLSQDMWQLDLSPGC 167

Db 121 WASGLETLDSLGTVLEASGYSTEVALSRQLGSLSQDMWQLDLSPGC 167

RESULT 7  
 AAB28448 Human OB polypeptide.

ID AAB28448 standard; protein; 167 AA.

XX DT 01-FEB-2001 (first entry)

XX PR 30-NOV-1994; 94US-00292345.

XX PR 10-MAY-1995; 94US-00347563.

XX PR 10-MAY-1995; 95US-00438431.

XX PA (UYRQ ) UNIV ROCKEFELLER.

XX PI Mafei M, Proenca R, Zhang Y, Friedman JM;

XX DR WPI; 2000-601556/57.

XX DR N-PDB; AAC62566.

XX PR Nucleic acid primers and probes useful for detecting mutations in mammalian OB gene associated with regulation of body weight and adiposity.

XX XX Example; Fig 3; 153pp; English.

XX The present sequence is encoded by a nucleotide sequence used in an invention relating to the control of body weight of animals including

CC CC humans. Nucleic acids of at least 10 nucleotides which are hybridizable

CC CC to a non-coding region of an OB nucleic acid have been created. The OB

CC CC gene plays a critical role in the regulation of body weight and

CC CC adiposity. The nucleic acids may be used as probes or as primers for PCR.

CC CC They are useful for evaluating the presence of mutations in the human OB

CC CC gene or for evaluating the level of expression of OB mRNA. Defects

CC associated with OB gene expression result in obese phenotypes  
 XX Sequence 167 AA;

Query Match 100.0%; Score 870; DB 3; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MHWGTLCGFLMWPLFVQAVPIQKVDQDTKLTKTIVRINDISHTQSVSSKOKVTGL 60  
 Db 1 MHWGTLCGFLMWPLFVQAVPIQKVDQDTKLTKTIVRINDISHTQSVSSKOKVTGL 60  
 Qy 61 DFIPGHPILTLSKMDQTLAVYQQILTSMSRPNVQISNDLNLDDLLHLYAFPSKSCHLP 120  
 Db 1 DFIPGHPILTLSKMDQTLAVYQQILTSMSRPNVQISNDLNLDDLLHLYAFPSKSCHLP 120  
 Qy 121 WASGLETLDSLGGVLEASGSTEVAVSRLOGSLQDMWLQDLSPEC 167  
 Db 121 WASGLETLDSLGGVLEASGSTEVAVSRLOGSLQDMWLQDLSPEC 167  
 Qy 121 WASGLETLDSLGGVLEASGSTEVAVSRLOGSLQDMWLQDLSPEC 167  
 Db 121 WASGLETLDSLGGVLEASGSTEVAVSRLOGSLQDMWLQDLSPEC 167

## RESULT 8

AYA84190 standard; protein; 167 AA.  
 XX DT 25-MAY-2000 (first entry)  
 AC DE Human obese OB protein SEQ ID NO:5.

XX DT 03-JUL-2000 (first entry)

XX DE Amino acid sequence of the primary structure of human leptin.

XX KW Human; leptin; blood brain barrier; homeostasis; body mass; anorexia; obesity; hyperglycemia; hyperinsulinemia; hyperphagia; thyroid dysfunction; infertility; type II diabetes mellitus; non-insulin-dependent diabetes mellitus; hematopoiesis dysfunction; tumour suppression; weight loss; diet.  
 XX OS Homo sapiens.  
 XX PN WO200011173-A1.

XX PD 02-MAR-2000.  
 XX PF 20-AUG-1999; 99WO-US019021.

XX PR 21-AUG-1998; 98US-1097457P.  
 PR 19-AUG-1999; 99US-00377081.  
 XX PA (ALBA-) ALBANY MEDICAL COLLEGE.

XX PI Grasso P, Lee DW, Leinung MC;  
 XX DR; 2000-237652/20.  
 XX PT Leptin peptides useful for treating pathophysiology relating to homeostasis of body mass such as obesity, anorexia, and hematopoiesis dysfunction and tumor suppression.

XX PS Claim 26: Fig 16; 121pp; English.

XX The present sequence represents a human leptin. The specification describes peptides derived from leptin. The leptin-derived peptides have increased ability to cross the blood brain barrier and improved bioavailability. Peptides derived from leptin are useful for treating and preventing pathophysiology relating to homeostasis of body mass such as anorexia, obesity, comprising hyperglycemia, hyperinsulinemia, hyperphagia, thyroid dysfunction, infertility, type II diabetes mellitus, and non-insulin-dependent diabetes mellitus (NIDDM), and hematopoiesis dysfunction and tumor suppression. The peptides are also useful for identifying drugs useful in weight loss diet regimen  
 XX Sequence 167 AA;  
 SQ Query Match 100.0%; Score 870; DB 3; Length 167;

Query Match 100.0%; Score 870; DB 3; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MHWGTLCGFLMWPLFVQAVPIQKVDQDTKLTKTIVRINDISHTQSVSSKOKVTGL 60  
 Db 1 MHWGTLCGFLMWPLFVQAVPIQKVDQDTKLTKTIVRINDISHTQSVSSKOKVTGL 60  
 Qy 61 DFIPGHPILTLSKMDQTLAVYQQILTSMSRPNVQISNDLNLDDLLHLYAFPSKSCHLP 120  
 Db 61 DFIPGHPILTLSKMDQTLAVYQQILTSMSRPNVQISNDLNLDDLLHLYAFPSKSCHLP 120  
 Qy 121 WASGLETLDSLGGVLEASGSTEVAVSRLOGSLQDMWLQDLSPEC 167  
 Db 121 WASGLETLDSLGGVLEASGSTEVAVSRLOGSLQDMWLQDLSPEC 167  
 Qy 121 WASGLETLDSLGGVLEASGSTEVAVSRLOGSLQDMWLQDLSPEC 167  
 Db 121 WASGLETLDSLGGVLEASGSTEVAVSRLOGSLQDMWLQDLSPEC 167

## RESULT 9

AYA80259 standard; protein; 167 AA.  
 XX ID AY80259  
 XX AC AY80259;  
 XX DT 25-MAY-2000 (first entry)  
 XX DE Human obese OB protein SEQ ID NO:5.

XX KW Obesity; OB protein; polyethylene; Polypropylene; weight; obesity;  
 KW anorectic; gene therapy; type II diabetes mellitus; hypertension;  
 KW hyperlipidaemia.  
 XX OS Homo sapiens.  
 XX FH Location/Qualifiers  
 XX FT 1..21  
 XX FT /label= signal  
 XX FT 23..167  
 XX FT /label= OB\_protein  
 XX PN US605325-A.  
 XX PD 15-FEB-2000.  
 XX PF 15-MAY-1996; 96US-00648263.  
 XX PR 05-MAY-1995; 95US-0045777.  
 PR 07-JUN-1995; 95US-00434629.  
 XX PA (HOFF ) HOFFMANN LA ROCHE INC.  
 XX PI Guibez Y, Campfield A, Devos R;  
 XX DR; 2000-194674/17.  
 DR N-PSDB; AAZ91516.  
 XX Disclosure; Col 39-40; 29pp; English.

XX The present invention describes polyethylene glycol conjugated obese (OB) protein compositions (1) useful for modulating the body weight of humans and animals for the prevention, treatment and control of obesity and associated diseases. (1) have anorectic activity and can be used in gene therapy. (1) may be used for the prevention, treatment and control of obesity and associated diseases such as type II diabetes mellitus, hypertension and hyperlipidaemia. The present sequence represents the human OB protein, which can be used in the production of (1)  
 XX Sequence 167 AA;  
 SQ Query Match 100.0%; Score 870; DB 3; Length 167;

QY	1	MHNGTLCGFLWMPYLFFYQAVPIQVDDTKTLIKITVTRINDISHTQSSSKQKVYGL 60	Db	1	MHWGTLCGFLWMPYLFFYQAVPIQVDDTKTLIKITVTRINDISHTQSSSKQKVYGL 60
Db	1	MHNGTLCGFLWMPYLFFYQAVPIQVDDTKTLIKITVTRINDISHTQSSSKQKVYGL 60	Qy	61	DFIPGLHPILTLISKMDQTLAVYQQLTMSRNPNTQISNDLLENRLDHLVLAFTSKSCHLP 120
Qy	61	DFIPGLHPILTLISKMDQTLAVYQQLTMSRNPNTQISNDLLENRLDHLVLAFTSKSCHLP 120	Db	61	DFIPGLHPILTLISKMDQTLAVYQQLTMSRNPNTQISNDLLENRLDHLVLAFTSKSCHLP 120
Db	61	DFIPGLHPILTLISKMDQTLAVYQQLTMSRNPNTQISNDLLENRLDHLVLAFTSKSCHLP 120	Qy	121	WASGLLETDSLGGVLEASGYSTEVALSRLOGSLQDMWLQDLSPGC 167
Qy	121	WASGLLETDSLGGVLEASGYSTEVALSRLOGSLQDMWLQDLSPGC 167	Db	121	WASGLLETDSLGGVLEASGYSTEVALSRLOGSLQDMWLQDLSPGC 167
Db	121	WASGLLETDSLGGVLEASGYSTEVALSRLOGSLQDMWLQDLSPGC 167			RESULT 11
			ID	AAB28467	standard; protein; 167 AA.
			XX	AAB28467;	
			ID	AAY87726	standard; protein; 167 AA.
			XX	AAY87726	
			AC	AAV87726;	
			XX	18-AUG-2000	(first entry)
			DR	DE	
			XX	Murine OB Protein #2.	
			XX	KW	OB gene; body weight; obesity; anorectic; adipose tissue; brain; murine.
			OS	OS	
			XX	Mus sp.	
			PN	US6048837-A.	
			XX	11-APR-2000.	
			PD	07-JUN-1995;	95US-00488214.
			XX	PF	
			XX	07-JUN-1995;	95US-00485942.
			XX	PR	17-AUG-1994;
			PR	17-AUG-1994;	94US-00292345.
			PR	30-NOV-1994;	94US-00347563.
			PR	10-MAY-1995;	95US-00438431.
			XX	PA	(UYRQ ) UNIV ROCKEFELLER.
			XX	PA	Proenca R, Zhang Y, Friedman JM;
			XX	PI	
			XX	PI	WPI; 2000-611018/58.
			XX	DR	N-PSDB; AAC62646.
			XX	XX	Novel antibody to mammalian obesity polypeptide useful for diagnosis and treatment of weight loss associated with disorders such as cancer, AIDS and anorexia nervosa.
			PS	XX	Claim 2; Fig 3; 150pp; English.
			PS	XX	The nucleotide sequence encoding the present protein was used in an invention relating to the control of body weight of animals including humans. Antibodies against the mammalian obesity (OB) polypeptide have been identified. The antibodies are useful for modulating the activity of OB to control body weight and fat content and/or to treat certain pathological conditions in which there is abnormal depression or elevation of body weight. The antibodies are used to treat weight loss associated with cancer, AIDS and anorexia nervosa. They are useful for the diagnosis of nutritional disorders such as obesity and diseases associated with obesity, such as hypertension, heart disease and Type II diabetes. The kits are used to determine the presence or amount of OB in the blood or plasma of an individual
			SQ	SQ	Sequence 167 AA;
			SQ	1	Query Match 100.0%; Score 870; DB 3; Length 167;
			SQ	Best Local Similarity 100.0%; Pred. No. 4.8e-85;	Best Local Similarity 100.0%; Pred. No. 4.8e-85;
			SQ	Mismatches 0; Mismatches 0;	Mismatches 0; Mismatches 0;
			Db	1	Query Match 100.0%; Score 870; DB 3; Length 167;
			Db	1	Best Local Similarity 100.0%; Pred. No. 4.8e-85;
			Qy	1	MHWGTLCGFLWMPYLFFYQAVPIQVDDTKTLIKITVTRINDISHTQSSSKQKVYGL 60
			Qy	1	MHWGTLCGFLWMPYLFFYQAVPIQVDDTKTLIKITVTRINDISHTQSSSKQKVYGL 60

Qy 61 DFIGLHPILTSKMDQTLLAYQQILTSMPSRNVIOISNDLENRLDLLVLAFSKSCHLP 120  
 61 DFIGLHPILTSKMDQTLLAYQQILTSMPSRNVIOISNDLENRLDLLVLAFSKSCHLP 120  
 Db 61 DFIGLHPILTSKMDQTLLAYQQILTSMPSRNVIOISNDLENRLDLLVLAFSKSCHLP 120  
 DE Human leptin.  
 XX  
 Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRLGSQDMWQLDLSPGC 167  
 121 WASGLETLDSLGGVLEASGYSTEVALSRLGSQDMWQLDLSPGC 167  
 Db 121 WASGLETLDSLGGVLEASGYSTEVALSRLGSQDMWQLDLSPGC 167  
 DE Human leptin.  
 XX  
 RESULT 12  
 AAB53914 standard; protein; 167 AA.  
 XX  
 AC AAB53914;  
 XX DT 06-JUN-2001 (first entry)  
 DE Human leptin fragment SEQ ID NO: 32.  
 XX  
 KW Leptin; human; LSR; lipolysis stimulated receptor; obesity; hypertension;  
 KW anorexia; cachexia; stroke; atherosclerosis.  
 XX  
 OS Homo sapiens.  
 PN WO200121647-A2.  
 XX  
 PD 29-MAR-2001.  
 XX  
 PP 22-SEP-2000; 2000WO-IB001470.  
 PR 22-SEP-1999; 99US-0155506P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Yen F, Erickson MR, Truebis J, Bihain B;  
 XX  
 DR 2001-218642/22.  
 XX  
 PT New leptin polypeptide fragment and related polynucleotides, useful for  
 PT the prevention and treatment of obesity and obesity-related diseases such  
 PT as hypertension and diabetes.  
 XX  
 PS Claim 1; Page 232-233; 247PP; English.  
 XX  
 CC The present invention provides the protein and coding sequences of leptin  
 CC fragments which modulate the activity of lipolysis stimulated factor  
 CC (LSR). These sequences are useful in the treatment of obesity related  
 CC diseases, including obesity, anorexia, cachexia, cardiac and coronary  
 CC insufficiency, stroke, hypertension, atherosomatic disease,  
 CC atherosclerosis, non-insulin dependent diabetes, hyperlipidaemia,  
 CC hypertriglyceridaemia and syndrome X.  
 XX  
 SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 4; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-85; Mismatches 0; Indels 0; Gaps 0;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLICGFLMLWPYLFLYQAVPIQKVQDDTKLTKITIVTRINDISHTQSVSQSKOKVTGL 60  
 1 MHWGTLICGFLMLWPYLFLYQAVPIQKVQDDTKLTKITIVTRINDISHTQSVSQSKOKVTGL 60  
 Db 1 MHWGTLICGFLMLWPYLFLYQAVPIQKVQDDTKLTKITIVTRINDISHTQSVSQSKOKVTGL 60  
 DE Human leptin (LEP).  
 XX  
 Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRLGSQDMWQLDLSPGC 167  
 121 WASGLETLDSLGGVLEASGYSTEVALSRLGSQDMWQLDLSPGC 167  
 Db 121 WASGLETLDSLGGVLEASGYSTEVALSRLGSQDMWQLDLSPGC 167  
 DE Human leptin (LEP).  
 XX  
 KW Mucosal cell; cell therapy; gene therapy; hyperglycaemia; wound healing;  
 KW haemophilia; eye damage; diabetes; obesity; degenerative disorder; ulcer;  
 KW beta-cell destruction; kidney tubule calcification; liver degeneration;

AAB72927  
 ID AAB72927 standard; protein; 167 AA.  
 XX  
 AC AAB72927;  
 XX DT 16-MAY-2001 (first entry)  
 DE Human leptin.  
 XX  
 KW Bone resorption modulation; leptin; osteoporosis; Paget's disease;  
 KW osteoclastogenesis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN AU200048971-A.  
 XX  
 PD 08-FEB-2001.  
 XX  
 PP 01-AUG-2000; 2000AU-00048971.  
 PR 03-AUG-1999; 99AU-00001999.  
 XX  
 PA (UTME ) UNIV MELBOURNE.  
 XX  
 PI Nicholson GC;  
 XX  
 DR 2001-235416/25.  
 XX  
 N-PSDB; AAF76769.  
 XX  
 PT Modulating bone resorption in human or animal for treating osteoporosis  
 PT or Paget's disease, comprises administering leptin, its derivative,  
 PT homologue, analog, chemical equivalent, antagonist or agonist.  
 XX  
 PS Claim 3; Page 26-27; 40pp; English.  
 XX  
 CC The present invention describes a method of modulating bone resorption  
 CC comprising administering leptin or a derivative under conditions suitable  
 CC for the modulation of osteoclastogenesis. This is useful in the treatment  
 CC of osteoporosis and Paget's disease. The present sequence is the human  
 CC leptin protein sequence  
 XX  
 SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 4; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-85; Mismatches 0; Indels 0; Gaps 0;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLICGFLMLWPYLFLYQAVPIQKVQDDTKLTKITIVTRINDISHTQSVSQSKOKVTGL 60  
 1 MHWGTLICGFLMLWPYLFLYQAVPIQKVQDDTKLTKITIVTRINDISHTQSVSQSKOKVTGL 60  
 Db 1 MHWGTLICGFLMLWPYLFLYQAVPIQKVQDDTKLTKITIVTRINDISHTQSVSQSKOKVTGL 60  
 DE Human leptin (LEP).  
 XX  
 Qy 61 DFIGLHPILTSKMDQTLLAYQQILTSMPSRNVIOISNDLENRLDLLVLAFSKSCHLP 120  
 61 DFIGLHPILTSKMDQTLLAYQQILTSMPSRNVIOISNDLENRLDLLVLAFSKSCHLP 120  
 Db 61 DFIGLHPILTSKMDQTLLAYQQILTSMPSRNVIOISNDLENRLDLLVLAFSKSCHLP 120  
 DE Human leptin (LEP).  
 XX  
 Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRLGSQDMWQLDLSPGC 167  
 121 WASGLETLDSLGGVLEASGYSTEVALSRLGSQDMWQLDLSPGC 167  
 Db 121 WASGLETLDSLGGVLEASGYSTEVALSRLGSQDMWQLDLSPGC 167  
 DE Human leptin (LEP).  
 XX  
 KW Mucosal cell; cell therapy; gene therapy; hyperglycaemia; wound healing;  
 KW haemophilia; eye damage; diabetes; obesity; degenerative disorder; ulcer;  
 KW beta-cell destruction; kidney tubule calcification; liver degeneration;

KW diabetic retinopathy; cancer; coronary heart disease; growth disorder;  
 KW dyslipidaemia; coagulation disorder; stroke; peripheral vascular disease;  
 KW hypertension; wasting syndrome; passive immunization; immunosuppressive;  
 KW Helicobacter pylori; arthritis; cardiovascular disease; ophthalmological;  
 KW hypoglycaemic; anorectic; coagulant; cerebroprotective; antimicrobial;  
 KW lepto; LBP; pulmonary; cytostatic; hypotensive; cardiant; human;  
 KW OS Homo sapiens.  
 XX WO200168828-A2.  
 XX PD 20-SEP-2001.  
 XX PF 12-MAR-2001; 2001WO-IB000722.  
 PR 13-MAR-2000; 2000US-0188796P.  
 PR 08-DEC-2000; 2000US-0254464P.  
 PA (ENGE-) ENGENE INC.  
 XX PT Kieffer TJ, Cheung AT;  
 XX DR WPI: 2001-582445/65.  
 DR N-PSDB; AAD17487.  
 XX PT Novel isolated or cultured mucosal cell producing nutrient-regulatable  
 PR protein expressed by transgene comprising expression control element  
 PR linked with nucleic acid encoding protein, is useful for treating  
 PR diabetes.  
 XX Disclosure; Fig 17; 75pp; English.  
 PS The present invention relates to an isolated or cultured mucosal cell  
 CC that produces a protein regulatable by a nutrient, where expression of  
 CC the protein is conferred by a transgene comprising an expression control  
 CC element in operable linkage with nucleic acid encoding the protein. The  
 CC invention is used in cell therapy and gene therapy. Isolated or cultured  
 CC mucosal cell is useful for treating a hyperglycaemic condition such as  
 CC type I diabetes (insulin-dependent diabetes), where the subject has a  
 CC fasting plasma glucose level of greater than 110 mg/dl. It is also useful  
 CC for treating obesity or undesirable body mass. Preferably, in these  
 CC conditions the mucosal cell expresses insulin, leptin, glucagon-like  
 CC peptide (GLP)-1, GIP<sub>2</sub>, cholecystokin (CCK), a glucagon antagonist,  
 CC growth hormone, a clotting factor or an antibody. The mucosal cells are  
 CC implanted into a mucosal tissue or non-mucosal tissue such as liver,  
 CC pancreas or muscle. Mice strains that develop or are susceptible to  
 CC developing a particular disease (e.g. diabetes, cancer, degenerative  
 CC disorders etc.) are also useful for introducing therapeutic proteins in  
 CC order to study the effect of therapeutic protein expression in the  
 CC disease susceptible mouse. Mucosal cell is also useful for treating  
 CC insulin-independent (type 2) diabetes, degeneration of pancreas (beta-  
 CC cell destruction), kidney tubule calcification, degeneration of liver,  
 CC eye damage (diabetic retinopathy), diabetic foot, ulcerations in mucosa  
 CC such as mouth and gums, excess bleeding, wound healing or delayed blood  
 CC coagulation and increased risk of coronary heart disease, stroke,  
 CC peripheral vascular disease, dyslipidaemia, hypertension and obesity.  
 CC Macrophage cell also produces protein such as clotting factors to treat  
 CC haemophilia and other coagulation disorders, growth factors to treat  
 CC growth disorders or wasting syndrome, and antibodies to provide passive  
 CC immunisation or protection of a subject against foreign antigens or  
 CC pathogens e.g. Helicobacter pylori or to provide treatment of cancer,  
 CC arthritis, or cardiovascular disease. The present sequence is human  
 XX Sequence 167 AA;  
 SQ Query Match 100.0%; Score 870; DB 4; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MHWGTLGFLNTPWPLFYQAVPIQKVOQDTKLIKTVTRINDISHTQSVSQKQRTG 60  
 DB 1 MHWGTLGFLNTPWPLFYQAVPIQKVOQDTKLIKTVTRINDISHTQSVSQKQRTG 60

QY 61 DPIPGLHPILITSKMDQTLAVYQQUTSMSPRNVQISNDLENLRLHLVAFSSKSCHLP 120  
 Db 61 DPIPGLHPILITSKMDQTLAVYQQUTSMSPRNVQISNDLENLRLHLVAFSSKSCHLP 120  
 QY 121 WASGLELTDLSGGVLEASGYSTEVALSRLQGSQDMLWQDLSPGC 167  
 Db 121 WASGLELTDLSGGVLEASGYSTEVALSRLQGSQDMLWQDLSPGC 167

XX RESULT 15  
 AAU02890  
 ID AAU02890 standard; protein; 167 AA.  
 XX AC AAU02890;  
 XX ANU02890;  
 XX 12-SEP-2001 (first entry)  
 DT 12-SEP-2001  
 XX Human Ob protein sequence.  
 DE Human  
 KW Ob; haematopoietic cytokine; metabolism; weight regulation; inflammation;  
 KW appetite regulation; mammalian circulatory system; autoimmunity; cancer;  
 KW immunological response; abnormal proliferation; regeneration; human;  
 KW degeneration; responsive cell type atrophy.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 PH 1. .21  
 FT Peptide /note= "Signal peptide"  
 FT Protein 22. .167 "Mature human Ob protein"  
 FT /note= "Mature human Ob protein"  
 XX US6225446-B1.  
 PN  
 XX PD 01-MAY-2001.  
 XX PP 05-DEC-1996;  
 XX PR 06-DEC-1995;  
 XX PA (SCHEMING CORP.  
 PI Altmann SW, Rock FL, Bazan JF, Kastelein RA;  
 DR WPI; 2001-32/467/34.  
 XX PT Mutational variants of mammalian Ob proteins, useful e.g. for regulating  
 PT weight and appetite, also in screening or treatment of conditions  
 PT associated with abnormal proliferation.  
 XX Disclosure; Col 3-4; 24pp; English.  
 PS The sequence represents human Ob protein which belongs to the  
 CC haematopoietic cytokine subgroup. Cytokines function in regulating  
 CC metabolism and weight by mediating differentiation and other signals  
 CC within the mammalian circulatory system. Pure or recombinant mutational  
 CC variants of mammalian Ob proteins may therefore be used for the  
 CC regulation of weight and appetite. These mutants and antibodies  
 CC that are useful in screening and treatment of conditions associated with  
 CC abnormal proliferation, such as cancer, and are of use in situations  
 CC where cytokine functions have been implicated, e.g. immunological  
 CC responses, inflammation, autoimmunity, regeneration and  
 CC degeneration of responsive cell types.  
 XX SQ Sequence 167 AA;  
 SQ Query Match 100.0%; Score 870; DB 4; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MHWGTLGFLNTPWPLFYQAVPIQKVOQDTKLIKTVTRINDISHTQSVSQKQRTG 60  
 DB 1 MHWGTLGFLNTPWPLFYQAVPIQKVOQDTKLIKTVTRINDISHTQSVSQKQRTG 60

Db 1 MHWGTLCLGFLMLWPYLFLYQAVPIQRKVQDDITKTLIKTIIVRINDISHTQSVSSTKQKVTLGL 60  
Qy 61 DFTPGLHPLTSLSKMDOQITLAVYQQITMSMPSRNVIOIQISNDLENLRDLHVLAPESSCHLP 120  
Db 61 DFTPGLHPLTSLSKMDOQITLAVYQQITMSMPSRNVIOIQISNDLENLRDLHVLAPESSCHLP 120  
Qy 121 WASGLETLDSUGGVLEASGYSTEVALSRLQGSLSQDMLWQDLSPEC 167  
Db 121 WASGLETLDSUGGVLEASGYSTEVALSRLQGSLSQDMLWQDLSPEC 167

Search completed: March 12, 2005, 04:59:47  
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Scoring table:	BLOSUM62	Alignments:		
Searched:	1612378 seqs, 512079187 residues			
Total number of hits satisfying chosen parameters:	1612378			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0% Maximum Match 100%			
Database :	UniProt 03: 1: uniprot_sprot: 2: uniprot_trembl: *			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES	%			
Result No.	Score	Query	Description	
Match	Length	DB	ID	
-	-	-	-	
1	870	100.0	OB_HUMAN	P41159 homo sapien
2	866	99.5	167	1 Q6NT58 homo sapien
3	780	89.7	167	1 OB_MACMU macaca mulatta
4	723	84.3	146	1 OB_PANT pan troglodytes
5	728	83.7	146	1 OB_GORGO gorilla gorilla
6	724	83.2	167	1 OB_FELCA felis silvestris
7	721	82.9	146	1 OB_PONPY pongo pygmaeus
8	715	82.2	167	1 OB_PIG sus scrofa
9	705	81.0	167	1 OB_BOVIN bos taurus
10	704	80.9	167	1 OB_MOUSE mus musculus
11	690	79.3	167	1 OB_RAT rattus norvegicus
12	675	77.6	167	1 OB_CANFA canis familiaris
13	640	73.6	163	1 OB_CHICK gallus gallus
14	628	72.2	146	1 OB_SHEEP ovis aries
15	624	71.7	146	1 OB_BOVIN
16	588.5	67.6	145	2 OB_EQUI equus caballus
17	576.5	66.3	145	2 OB_MELGA meleagris gallopavo
18	551	63.3	167	1 OB_SMICR smithiopsis
19	535	61.5	167	2 Q706D0 halichoeretus leucocephalus
20	535	61.5	167	2 Q706D1 phoca vitulina
21	498	57.2	119	2 Q861R2 bubalus bubalis
22	481	55.3	123	2 Q95K9 myotis lucifugus
23	477	54.8	118	2 Q8MK60 alopex lagurus
24	476	54.7	118	2 Q8MK58 vulpes vulpes
25	474	54.5	118	2 Q8MK59 nyctereutes leucoticus
26	469	53.9	118	2 Q8MK61 canis familiaris
27	449	51.6	109	2 Q866S7 bubalus bubalis
28	447	51.4	99	1 OB_HORSE equus caballus
29	439	50.5	109	2 Q864V1 camelus dromedarius
30	387	44.5	106	2 Q95MGS capra hircus
31	380	43.7	90	2 Q8WMK7 delphinapterus leucas

- RA Niki T., Mori H., Tamori Y., Kishimoto-Hashiramoto M., Ueno H.,  
 RA Araki S., Masugi J., Sawant N., Majithia R., Rais N.;  
 RA Hashiramoto M., Taniguchi H., Kasuga M.;  
 RT "Human obese gene: molecular screening in Japanese and Asian Indian  
 NIDDM patients associated with obesity.";  
 RL Diabetes 45:675-678(1996). ;  
 RP SEQUENCE FROM N.A.  
 RA Lu L., Fu Z., Xu M., Fu Y., Hu Z.;  
 RN Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.  
 [9]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=placenta;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.D., Collins F.S., Wagner R.L., Schaefer C.M., Schulter G.D.,  
 RA Altchul S.F., Zebeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J.J., Hsieh F.,  
 RA Diatchenko L., Matsusita K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Benaldo M.P., Cesavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S., Loqueline N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McCorman K.J., Malek J.A., Gunarstne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Rodgeron K., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimes J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schniech A., Schein J.E., Jones S.J.M., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [10]  
 RP INTERACTION WITH SIGLEC6.  
 RX MEDLINE=9357812; PubMed=10428856; DOI=10.1074/jbc.274.32.227229;  
 RA Patel N., Brinkman-Van der Linden B.C.M., Altmann S.W., Gish K.C.,  
 RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,  
 RA Varki A., Kastellein R.A.;  
 RT "OB-BP1/Siglec-6: A leptin- and sialic acid-binding protein of the  
 immunoglobulin superfamily.";  
 RT "Leptin is a four-helix bundle: secondary structure by NMR.";  
 RN [11]  
 RP ERRATUM.  
 RA Patel N., Brinkman-Van der Linden B.C.M., Altmann S.W., Gish K.C.,  
 RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,  
 RA Varki A., Kastellein R.A.;  
 RL J. Biol. Chem. 274:22729-22738(1999).  
 [12]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=7303492; PubMed=9166907; DOI=10.1016/S0014-5793(97)00353-0;  
 RA Kline A.D., Becker G.W., Churgay L.M., Landen B.E., Martin D.K.,  
 RA Muth W.L., Rathnachalam R., Richardson J.M., Schonier B., Ulmer M.,  
 RA Hale J.E.;  
 RT "Leptin is a four-helix bundle: secondary structure by NMR.";  
 RL FEBS Lett. 407:239-242(1997).  
 [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
 RX MEDLINE=97289390; PubMed=91442951;  
 RA Zhang F., Basinski M.B., Beilis J.M., Briggs S.L., Churgay L.M.,  
 RA Clawson D.K., Dimarchi R.D., Furman T.C., Hale J.E., Hsiung H.M.,  
 RA Schonier B.E., Smith D.P., Zhang X.Y., Wery J.P., Schevitz R.W.;  
 RL Nature 387:206-209(1997).  
 [14]  
 RP VARIANT MET-94.  
 RA Bartholomew D.W., McClellan J.M.;  
 RT "A novel polymorphism in the leptin gene.";  
 RL Hum. Mutat. 12:220-220(1998).  
 [15]  
 RP VARIANT MORBID OBESITY TRP-105.  
 RX MEDLINE=98160176; PubMed=9500540;
- RA Strobel A., Issad T., Camoin L., Ozata M., Strosberg A.D.;  
 RT "A Leptin missense mutation associated with hypogonadism and morbid  
 obesity.";  
 RT Nat. Genet. 18:213-215(1998).  
 RL -!- FUNCTION: May function as part of a signaling pathway that acts to  
 CC regulate the size of the body fat depot. An increase in the level  
 CC of LEP may act directly or indirectly on the CNS to inhibit food  
 CC intake and/or regulate energy expenditure as part of a homeostatic  
 CC mechanism to maintain constancy of the adipose mass.  
 CC -!- SUBUNIT: Interacts with SIGLEC6.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DISEASE: Defects in LEP may be a cause of autosomal recessive  
 CC -!- obesity [MIM:501665].  
 CC -!- SIMILARITY: Belongs to the leptin family.  
 CC -!- DATABASE: NAME=R&D Systems, cytokine mini-reviews; LEP;  
 CC -!- WWW=[http://www.rndsystems.com/asp/g\\_sitebuilder.asp?bodyId=213](http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=213).  
 CC -!- SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC -!- DR EMBL; U18915; AAA0470\_1; -.  
 CC -!- DR EMBL; D9487; BAA0848\_1; -.  
 CC -!- DR EMBL; U43653; AAC50400\_1; -.  
 CC -!- DR EMBL; U3415; AAC31660\_1; -.  
 CC -!- DR EMBL; D63710; BAA09839\_1; -.  
 CC -!- DR EMBL; D63709; BAA09839\_1; JOINED.  
 CC -!- DR EMBL; D63519; BAA09787\_1; -.  
 CC -!- DR EMBL; D63518; BAA09787\_1; JOINED.  
 CC -!- DR EMBL; AF008123; AAB63507\_1; -.  
 CC -!- DR EMBL; BC060830; AAH60830\_1; -.  
 CC -!- DR PIR; A38152; ITHU.  
 CC -!- DR PIR; I53166; I53166.  
 CC -!- DR GO; GO:0005615; C:extracellular space; TAS.  
 CC -!- DR GeneW; HGNC:6553; LEP.  
 CC -!- DR MIM; 601665; -.  
 CC -!- DR PDB; 1Ax8; X-ray; @=22-167.  
 CC -!- DR InterPro; IPR009079; 4\_helix\_cytokine.  
 CC -!- DR InterPro; IPR000055; Leptin.  
 CC -!- DR PFam; PF02024; Leptin\_1.  
 CC -!- DR PRINTS; PR00495; LEPTIN.  
 CC -!- DR PRODOM; PD005698; Leptin\_1.  
 CC -!- DR 3D-structure; Diabetes mellitus; Disease mutation; Obesity;  
 CC -!- DR Polymorphism; Signal.  
 CC -!- FT SIGNAL 1 21 Potential.  
 CC -!- FT CHAIN 22 Leptin.  
 CC -!- FT DISULFID 117 167 Hypogonadism.  
 CC -!- FT VARIANT 49 49 Missing (in 30% the clones).  
 CC -!- FT /FTID=VAR\_001196.  
 CC -!- FT V->M.  
 CC -!- FT /FTID=VAR\_0041197.  
 CC -!- FT R->W (in morbid obesity and  
 CC -!- FT hypogonadism).  
 CC -!- FT /FTID=VAR\_008094.  
 CC -!- FT V->M (in DBSNP:1800564).  
 CC -!- FT /FTID=VAR\_011955.  
 CC -!- FT Q->R (in Ref. 8).



Matches 150; Conservative 10; Mismatches 7; Indels 0; Gaps 0;  
 Qy 1 MHWGTLQGEFLWMPVLFYQAVPIKQVQDPTKTLIKTTIVTRINDISHTQSISKWTCI 60  
 :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 1 MYWRWLWGFMLWMPVLFYIQAVIDKQVSDTCKTLIKTTIVTRINDISHTQSISKWTCI 60  
 61 DFTPGHPLITLSKMDQTLLAVYQQLTSMSRNVTOISNDLENRLILVLAFLSKSCHP 120  
 Db 61 DFTPGHPLITLSKMDQTLLAVYQQLTSMSRNVTOISNDLENRLILVLAFLSKSCHP 120  
 RESULT 5  
 OB\_GORGO STANDARD; PRT; 146 AA.  
 ID OB\_GORGO  
 AC Q95189;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Leptin (Obesity factor).  
 Name=LEP; Synonyms=OB;  
 RN SEQUENCE FROM N.A.  
 OB Gorilla gorilla (Lowland gorilla).  
 RA Smith D.P., Zhang X., Hsiung H.M.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 NCBI TaxID=995;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP Smith D.P., Zhang X., Hsiung H.M.;  
 OB Gorilla gorilla (Lowland gorilla).  
 RA Smith D.P., Zhang X., Hsiung H.M., Zhang X.,  
 RN [1]  
 RP Schonher B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,  
 RA Rockey P.K., Rostek P.R.;  
 RT "Cloning of obese genes from different species: a comparison of the  
 gene structures and the sequences of the obese gene products,  
 RT leptin.";  
 RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.  
 -I- FUNCTION: May function as part of a signaling pathway that acts to  
 CC regulate the size of the body fat depot. An increase in the level  
 CC of LEP may act directly or indirectly on the CNS to inhibit food  
 CC intake and/or regulate energy expenditure as part of a homeostatic  
 CC mechanism to maintain constancy of the adipose mass (By  
 CC similarity).  
 -I- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -I- SIMILARITY: Belongs to the Leptin family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC or send an email to license@isb-sib.ch).  
 CC EMBL; U72872; AAB7091\_1; -.  
 DR HSSP; PA1159; 1AX8.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR Pfam; PRO2024; Leptin.  
 DR PRINTS; PR00495; LEPTIN.  
 DR ProDom; PDO05698; Leptin; 1.  
 KW Obesity.  
 FT DISULFID 96 146 By similarity.  
 SQ SEQUENCE 146 AA; 16058 MW; 02C42A0B554D55C CRC64;  
 DR Query Match 84.3%; Score 733; DB 1; Length 146;  
 DR Best Local Similarity 99.3%; Pred. No. 1.9e-58;  
 DR Matches 145; Conservative 1; Mismatches 0;  
 DR Indels 0; Gaps 0;  
 DR Disulfid 96 146 AA; 16058 MW; 02C42A0B554D55C CRC64;  
 DR Query Match 84.3%; Score 733; DB 1; Length 146;  
 DR Best Local Similarity 99.3%; Pred. No. 1.9e-58;  
 DR Matches 145; Conservative 1; Mismatches 0;  
 DR Indels 0; Gaps 0;  
 DR Disulfid 96 146 AA; 16058 MW; 02C42A0B554D55C CRC64;  
 DR Query Match 84.3%; Score 733; DB 1; Length 146;  
 DR Best Local Similarity 99.3%; Pred. No. 1.9e-58;  
 DR Matches 145; Conservative 1; Mismatches 0;  
 DR Indels 0; Gaps 0;  
 DR Disulfid 96 146 AA; 16058 MW; 02C42A0B554D55C CRC64;  
 DR Query Match 84.3%; Score 733; DB 1; Length 146;  
 DR Best Local Similarity 99.3%; Pred. No. 1.9e-58;  
 DR Matches 145; Conservative 1; Mismatches 0;  
 DR Indels 0; Gaps 0;  
 DR Disulfid 96 146 AA; 16058 MW; 02C42A0B554D55C CRC64;  
 DR Query Match 84.3%; Score 733; DB 1; Length 146;  
 DR Best Local Similarity 99.3%; Pred. No. 1.9e-58;  
 DR Matches 145; Conservative 1; Mismatches 0;  
 DR Indels 0; Gaps 0;  
 DR Disulfid 96 146 AA; 16058 MW; 02C42A0B554D55C CRC64;  
 DR Query Match 84.3%; Score 733; DB 1; Length 146;  
 DR Best Local Similarity 99.3%; Pred. No. 1.9e-58;  
 DR Matches 145; Conservative 1; Mismatches 0;  
 DR Indels 0; Gaps 0;  
 DR Disulfid 96 146 AA; 16058 MW; 02C42A0B554D55C CRC64;



Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.

[2] SEQUENCE FROM N.A.

RA Ramsay T.G.; Yan X.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

[3] SEQUENCE FROM N.A.

RC STRAIN=Landrace;

RA Robert C., Palin M.-P., Coulombe N., Roberge C., Silversides F.G., Benkert B.F., McKay R.M., Pelletier G.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

[4] SEQUENCE FROM N.A.

RC Bidwell C.A., Ji S.; Spurlock M.E.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

[5] SEQUENCE FROM N.A.

RC STRAIN=Meishan;

RA Dai R., Li N., Hu X., Wu C.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

[6] SEQUENCE FROM N.A.

RC McNeel R.L., Merriam H.J.; RT "Adipose tissue regulatory transcript expression in lean versus obese pigs"; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

[7] SEQUENCE FROM N.A.

RC STRAIN=Large white;

RA Soares M.A.M., Euclydes R.F., Guimaraes S.E.F., Martins M.P., Lopes P.S.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

[8] SEQUENCE OF 15-110 FROM N.A.

RC TISSUE=White adipose tissue; MEDLINE=971009821; PubMed=8856925; NEUENSWANDER S., Rettenberger G., Meijerink E., Jorg H., Stranzinger G.; RT "Partial characterization of porcine obesity gene (OBS) and its localization to chromosome 18 by somatic cell hybrids.";

RL Anim. Genet. 27:275-278(1996).

-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.

-!- SUBCELLULAR LOCATION: Secreted (Probable).

-!- SIMILARITY: Belongs to the leptin family.

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CC DR U63540; AAB05923.1; -

CC DR EMBL; U55894; AAB03458.1; -

CC DR EMBL; AF026976; AAB88274.1; -

CC DR EMBL; U66654; AAB97308.1; -

CC DR EMBL; AF0522691; AAC06303.1; -

CC DR EMBL; AF102856; AAC78147.1; -

CC DR EMBL; AF477387; AAC84792.1; -

CC DR EMBL; U40812; AAC86641.1; -

CC HSSP; P41159; LAX8

CC DR InterPro; IPR009079; 4\_helix\_cytokine.

CC DR InterPro; IPR000055; Leptin.

CC DR Pfam; PF02024; Leptin; 1.

CC DR PRINTS; PR0045; LEPTIN.

CC DR Prodom; PD005598; Leptin; 1.

CC KW Obesity; Signal.

-----

FT SIGNAL 1 21 Potential.

FT CHAIN 22 167 Leptin.

FT DISPLFID 117 167 BY similarity.

FT CONFLICT 21 22 AV -> GP (in Ref. 8).

FT CONFLICT 97 97 I -> L (in Ref. 8).

FT CONFLICT 122 122 A -> R (in Ref. 4).

SQ SEQUENCE 167 AA; 18861 MW; 27550BE0E63914E CRC64;

Query Match 82.2%; Score 715; DB 1; Length 167;

Best Local Similarity 85.0%; Pred. No. 9.7e-57;

Matches 142; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MHWGFLICGFILWIPXLYQAVPICKVQDFTKLUKTIVRINDISHTQSVSXSKOKVTGL 60

Db 1 MRCPGICRCPWLNWPLSYTAEVAPWRYQDFTKLUKTIVRINDISHTQSVSXSKOKVTGL 60

Qy 61 DFPIPLHPPLTLTSKMDQTLAVYQQLTSMPSRNVIQISNDLENRLDLHLVLAFLSKCHLP 120

Db 61 DFPIPLHPPLTLTSKMDQTLAVYQQLTSMPSRNVIQISNDLENRLDLHLVLAFLSKCHLP 120

Qy 121 WASGIETLPLDSLGGVLEASGYSTEVVALSRLQGSLQDMRLQDLSPGC 167

Db 121 QARALIETLSSLGGVLEASLYSTEVVALSRLQGALQDMRLQDLSPGC 167

RESULT 9

OB BOVIN STANDARD; PRT; 167 AA.

ID OB\_BOVIN

AC P50595; Q97918; Q97529;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Lepin precursor (Obesity factor).

GN Name=LEP; Synonyms=OB, OBS;

OS Bos taurus (Bovine);

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bos;

NCBI\_TaxID=9913;

OX [1]

RN SEQUENCE FROM N.A.

RP

RC TISSUE=Liver;

RA Tellam R.L., Briscoe S., Vuocolo A.;

CC CC Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

[2]

RN RN SEQUENCE OF 22-167 FROM N.A.

RP Ji S., Spurlock M.B.;

RT RT "Partial cloning of bovine obesity gene.";

RL RL Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.

[3]

RN RN SEQUENCE OF 22-167 FROM N.A.

RP RC TISSUE=White adipose tissue;

RA Kawakita Y., Abe H., Miyashige T.;

CC CC Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.

[4]

RN RN SEQUENCE FROM N.A., AND VARIANTS CYS-25 AND VAL-80.

RP RC MEDLINE=20036385; PubMed=10594227;

RA RA Lieffers S.C.; Konforcov B.A., Licence V.E., Miller J.R.;

RT RT "Genotype effects of bovine leptin mutations on pre- and postpartum lepin concentrations";

RL RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

[5]

RN RN SEQUENCE FROM N.A., AND VARIANT CYS-25.

RP RA Lien S., Sundvold H., Klingland H., Vaage D.I.;

RT RT "Two novel polymorphisms in the bovine obesity gene (OBS)." ;

RL RN SEQUENCE OF 46-145 FROM N.A.

RP RA Lien S., Sundvold H., Klingland H., Vaage D.I.;

RT RT "Two novel polymorphisms in the bovine obesity gene (OBS)." ;

RL Anim. Genet. 28:245-245 (1997).

Page 7

Qy	61 DFIGGLHPILTLSKMDQTLLAVYQQILTMSRPNVQISNDLENRLHLVLAFSKSCLLP 120	DR EMBL; U48849; AAC52514.1; -.
Db	61 DFIGGLHPILTLSKMDQTLLAVYQQILTMSRPNVQISNDLENRLHLVLAFSKSCLLP 120	DR PIR; PC034; ITRT.
Db	61 DFIGGLHPILTLSKMDQTLLAVYQQILTMSRPNVQISNDLENRLHLVLAFSKSCLLP 120	DR HSSP; PA4159; TAX8.
Qy	121 WASGLETDLSGGVL-EASLYSTEVALSRLQGSLQDMLWQDLSPGC 167	DR RGD; 3000; Lep.
Db	121 QTSGLKRPESLDGVLEASLYSTEVALSRLQGSLQDILQDLSPEC 167	DR InterPro; IPR009075; 4_helix_cytokine.
		DR InterPro; IPR000075; Leptin.
		PFam; PF02024; Leptin.
		PRINTS; PR00495; LEPTIN.
		DR Prodrom; PD00598; LEPTIN.
		DR ProDom; PD00598; Leptin.
		KW Obesity; Signal.
		KW Potential.
		FT SIGNAL; Signal.
		FT SIGNAL; 1 21
		FT PT Leptin.
		FT CHAIN 22 167
		FT DISLFID 117 167 By similarity.
		FT DISLFID 32 32 By similarity.
		FT CONFLICT 163 163 T (in Ref. 2).
		FT CONFLICT 163 163 L -> V (in Ref. 4).
		SQ SEQUENCE 167 AA; 18866 MW; 3B5B56DA42E84E CRC64;
		Query Match 79.3%; Score: 690; DB 1; Length: 167;
		Best Local Similarity 82.0%; Pred. No. 1.8e-54;
		Matches 137; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
Qy		YQ 1 MHWGFLCGFLWNLWLYFVYQAVPIQVQDDTKLTKITVTRINDIHSHTOSVSSKQKVTCGL 60
Db		YQ 1 MCWRPLCREFLWNLWSLYQAVPIHKVQDDTKLTKITVTRINDIHSHTOSVSAQRVTGGL 60
Qy		61 DFIPOLHPILTLSKMDQTLLAVYQQILTMSRPNVQISNDLENRLHLVLAFSKSCLLP 120
Db		61 DFIPOLHPILTLSKMDQTLLAVYQQILTMSRPNVQISNDLENRLHLVLAFSKSCLLP 120
Qy		61 WASGETLDSLGGVLEASGYSTEVALSRLQGSLQDMLWQDLSPEC 167
Db		61 QTRGLQKPESDLGVLEASLYSTEVALSRLQGSLQDILQDLSPEC 167
		[2]
		RESULT 12
		OB CANFA STANDARD; PRT; 167 AA.
		ID OB_CANFA ID OB_CANFA STANDARD; PRT; 167 AA.
		AC 002720; Q9TSG1; PRT; 167 AA.
		DT 15-JUL-1998 (Rel. 36, Created)
		DT 16-OCT-2001 (Rel. 40, Last sequence update)
		DT 25-OCT-2004 (Rel. 45, Last annotation update)
		DB Leptin precursor (Obesity factor).
		GN Name=LEP; Synonyms=OB;
		OS Canis familiaris (Dog).
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
		[1]
		RN NCBI_TaxID=9615;
		RN SEQUENCE FROM N.A.
		RC TISSUE=White adipose tissue;
		RA Iwae M., Sasaki N., Komagome R., Kimura K., Saito M.;
		OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
		[1]
		RN SEQUENCE FROM N.A.
		RC TISSUE=adipose tissue;
		RA Iwae M., Sasaki N., Komagome R., Kimura K., Saito M.;
		OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
		[1]
		RN SEQUENCE FROM N.A.
		RC TISSUE=adipose tissue;
		RA Smith D.P., Zhang X., Hsiung H.M.;
		CC Submitted (MAR-1977) to the EMBL/GenBank/DBJ databases.
		CC Submitted (MAR-1977) to the EMBL/GenBank/DBJ databases.
		CC -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of Lep may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.
		CC -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of Lep may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By
		CC -!- SIMILARITY: Belongs to the leptin family.
		CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
		CC -!- SUBCELLULAR LOCATION: Belongs to the leptin family.
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		CC DR D45162; BAA0896.1; -
		CC DR EMBL; S70586; AAB31657.2; -
		CC DR EMBL; D43653; BAA08529.1; -

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InterPro; IPR000065; Leptin.	DR EMBL; AF012777; AAC603661; 1;
Pfam; PF002049; LEPTIN.	DR EMBL; AF082500; AAC323801; -;
PRINTS; PR00495; LEPTIN.	DR HSSP; PA1159; 1AX8.
Prodom; PD005698; Leptin; 1.	DR InterPro; IPR009079; 4 helix_cytokine.
Obesity; Signal.	DR InterPro; IP000005; Leptin.
SIGNAL	DR Pfam; PP02024; Leptin; 1.
CHAIN	DR PRINTS; PR00495; LEPTIN.
DISULFID	DR ProDom; PD005698; Leptin; 1.
CONFLICT	DR KW Obesity; Signal.
SEQUENCE	FT SIGNAL 1 18 Potential.
167 AA;	FT CHAIN 19 163 Leptin.
18654 MW;	FT DISULFID 113 163 By Similarity.
9703CPBD2286A55 CRC64;	SQ SEQUENCE 163 AA; 18183 MW; 9F578D2528B18FC CRC64;
Query Match	Query Match 73.6%; Score 675; DB 1; Length 163;
Best Local Similarity	Best Local Similarity 79.0%; Pred. No. 5.8e-50;
Matches 134; Conservative 14; Mismatches 19;	Matches 132; Conservative 13; Mismatches 18; Indels 4; Gaps 2;
Indels 0; Gaps 0;	
1 MHEWGLTCFLWMPYLTFVQAVPTQKVDDDTKTLIKITIVTRINDISHTQSVSXKQVTGQ	Qy 1 MHNGTLCFLWMPYLTFVQAVPTQKVDDDTKTLIKITIVTRINDISHTQSVSXKQVTGQ
1 MRCGPCLCFWPLPSLVEAVPKVDDDTKTLIKITIVARINDISHTQSVSXKQRYAGL	Db 1 MCNRPLCR --LWSYLVYQAVPCQIFQDDDTKTLIKITIVTRINDISHT-SVSXKQVTGQ
61 DFIGLGLHPTLTKMDQTLAVYQQLTSMPSRNVIQISNDLENRLILHLAFLSKSCLP	Qy 61 DFIGLGLHPTLTKMDQTLAVYQQLTSMPSRNVIQISNDLENRLILHLAFLSKSCLP
61 DFIGLGLQPVLSRMDQTLAVYQQLNSLHSRNVIQISNDLENRLILHLAFLSKSCLP	Db 120
121 WAGGLETDLSLGVELEASYYSTEVVALSLRQLGSIQLDMWQDLSPGC	Qy 121 WAGGLETDLSLGVELEASYYSTEVVALSLRQLGSIQLDMWQDLSPGC
121 RARGLETFSLGGVLEASLYSTEVVANRLQAAQDMRLRDSPGC	Db 167
121 RARGLETFSLGGVLEASLYSTEVVANRLQAAQDMRLRDSPGC	Qy 121 RARGLETFSLGGVLEASLYSTEVVANRLQAAQDMRLRDSPGC
121 RARGLETFSLGGVLEASLYSTEVVANRLQAAQDMRLRDSPGC	Db 167
121 RARGLETFSLGGVLEASLYSTEVVANRLQAAQDMRLRDSPGC	Qy 121 RARGLETFSLGGVLEASLYSTEVVANRLQAAQDMRLRDSPGC
121 RARGLETFSLGGVLEASLYSTEVVANRLQAAQDMRLRDSPGC	Db 116

117 ONELOOPSINTERSTEVASLOGSODICLOUDSPEC  
118 RESULT 13

CHICK	OB CHICK	STANDARD;	PRT;	163 AA.
042164;				
15-JUL-1998 (Rel. 36)	15-JUL-1998 (Rel. 36, Last sequence update)			
25-OCT-2004 (Rel. 45, Last annotation update)	Leptin precursor (Obesity factor).			
Name=Lsp; Synonyms=OB;	Gallus gallus (Chicken).			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
NCBI_TaxID=9031;				
[1]	SEQUENCE FROM N.A. STRAIN=B-Boiler; TISSUE=Liver; MEDLINS=98201619; Published=9524275; DOI=10.1016/S0378-1119(97)006670-7; Taouis M., Chen J. W., Daviaud C., Dupont J., Derouet M., Simon J. ; "Cloning the chicken leptin gene."; Gene 208: 239-242 (1998).			
[2]	SEQUENCE FROM N.A. STRAIN=Shaver; TISSUE=Adipose tissue, and Liver; Ashwell C.M., Czerwinski S.M., McMurry J.P.; Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases. - FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By similarity). - SUBCELLULAR LOCATION: Secreted (Probable). - TISSUE SPECIFICITY: Not exclusively localized in adipose tissue but is also expressed in liver. - SIMILARITY: Belongs to the leptin family.			
RESULT 14				
Q678R8	PRELIMINARY;			
ID Q678R8;				
AC Q678R8;				
DT 05-JUL-2004 (TREMBLrel. 27, Created)				
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DE Leptin (Protein).				
OS <i>Bubalus bubalis</i> (Domestic water buffalo).				
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bovidae; Bubalidae; Bubalus.				
OC NCBI_TaxID=89462;				
OX				
RN [1]	SEQUENCE FROM N.A. TISSUE=adipose tissue; RA Rajendran S., Shukla D. C., Saravanan B.C. ; RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases. EMBL: AY427959; AAC05862.1; - . DR HSSP; PA1159; 1AKS.			
DR GO:0005516; C:extracellular; IEA.				
DR GO:0005179; F:hormone activity; IEA.				
DR GO:0007165; P:signal transduction; IEA.				
DR InterPro: IPR009079; 4 helix_cytokine.				
DR InterPro: IPR00065; Leptin.				
DR Pfam: PF02024; Leptin.				
DR PRINTS: PR00495; LEPTIN.				
DR ProDom: PD005698; Leptin.				
FT NON_TER 1 1				
FT CHAIN <1 1				
FT leptin.				
SEQUENCE 146 AA;	Score 628;	DB 2;	Length 146;	
SEQUENCE 146 AA;	Score 609 MW;	DB 2;	Length 146;	
Best Local Similarity 87.0%;	Pred. No. 6.1e-49;			
Matches 127;	Conservative 10;	Mismatches 9;	Indels 0;	Gaps 0;

Qy 22 VPIRKVQDDTKLTIKTVTRINDISHTQSVSQKRVTGDFIPGHPIITLSKMDQTLAV 81  
 Db 1 VPIRKVQDDTKLTIKTVTRINDISHTQSVSQKRVTGDFIPGHPIITLSKMDQTLAV 60

Qy 82 YQQILTSMPSRNVIQISNDIENLRDLHVLAFSKSCHLPPASGLETLDSIGGYLEASGYS 141  
 Db 61 YQQILTSLPSRNVVQISNDIENLRDLHVLIAASKSCPLPQYRALESLSIGVLEASLVS 120

Qy 142 TEVVALSRQLQSSLQDMRLQDLSLSPGC 167  
 Db 121 TEVVALSRQLQSSLQDMRLQDLSLSPGC 146

## RESULT 15

OB\_SHEEP ID OB\_SHEEP STANDARD; PRT; 146 AA.

AC Q28603; P79212; 01-NOV-1997 (Rel. 35, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Leptin (Obesity factor).

GN Name=LEP; Synonyms=OB;

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Caprinae; Ovis.

NCBI\_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Adipose tissue;

RA Simmons J.M., Dyer C.J., Keisler D.H.<sup>i</sup>, Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 9-125 FROM N.A.

RC TISSUE=Adipose tissue;

RX MEDLINE=98006799; PubMed=9347250; DOI=10.1016/S0739-7240(97)00028-3;

RA Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.<sup>i</sup>;

RT "cDNA cloning and tissue-specific gene expression of ovine leptin,

RT NPY-Y1 receptor, and NPY-Y2 receptor".

RL Domest. Anim. Endocrinol. 14:95-103 (1997).

-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.

-!- SUBCELLULAR LOCATION: Secreted (Protein family).

CC -!- SIMILARITY: Belongs to the leptin family.

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DR EMBL; UBA1247; AAB41786; 1.

DR EMBL; U62123; AAB51033; 1; -.

DR HSSP; PA1159; 1AXB.

DR InterPro; IPR009079; 4\_helix\_cytokine.

DR InterPro; IPR0065; Leptin.

DR Pfam; PF02024; Leptin; 1.

DR PRINTS; PR0049; LEPTIN.

DR PRO05598; Leptin; 1.

DR Obesity.

FT DISULFID 96 146 By similarity.

FT CONFLICT 65 65 L -&gt; H (In Ref. 2).

FT CONFLICT 92 92 A -&gt; G (In Ref. 2).

FT CONFLICT 124 124 V -&gt; L (In Ref. 2).

SEQUENCE 146 AA; 16053 MN; 19D54C324066CA CRC64;

SQ Query Match Similarity 71.7%; Score 624; DB 1; Length 146;

Best Local Similarity 87.0%; Pred. No. 1.4e-48;

Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 22 VPIRKVQDDTKLTIKTVTRINDISHTQSVSQKRVTGDFIPGHPIITLSKMDQTLAV 81

Db 1 VPIRKVQDDTKLTIKTVTRINDISHTQSVSQKRVTGDFIPGHPIITLSKMDQTLAV 60

Qy 82 YQQILTSMPSRNVIQISNDIENLRDLHVLAFSKSCHLPPASGLETLDSIGGYLEASGYS 141

Db 61 YQQILTSLPSRNVVQISNDIENLRDLHVLIAASKSCPLPQYRALESLSIGVLEASLVS 120

Qy 142 TEVVALSRQLQSSLQDMRLQDLSLSPGC 167

Db 121 TEVVALSRQLQSSLQDMRLQDLSLSPGC 146

Search completed: March 12, 2005, 05:03:38

Job time : 122.581 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:44:03 ; Search time 109.15 Seconds  
 (without alignments)  
 517.333 Million cell updates/sec

Title: US-10-049-182-6  
 Perfect score: 736  
 Sequence: 1 VPPIQKVQDDTKTLLIKTIVR.....SRIQGSIQDMLWQLDLSPGC 146

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2105632 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:  
 1: geneseqp1980s:  
 2: geneseqp1980s:  
 3: geneseqp2006s:  
 4: geneseqp2001s:  
 5: geneseqp2002s:  
 6: geneseqp2003s:  
 7: geneseqp2003bs:  
 8: geneseqp2004s:  
 9: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	%	Match	Length	DB	ID	Description
1	736	100.0	146	2	AAW00013	Aaw00013		Acid stab
2	736	100.0	146	2	AAW99490	Aar99490		Chimeric
3	736	100.0	146	2	AAW00539	Aaw00539		Human mat
4	736	100.0	146	2	AAW30892	Aaw30892		Synthetic
5	736	100.0	146	2	AAW34482	Aaw34482		Human obe
6	736	100.0	146	2	AAW10151	Aaw10151		Properly
7	736	100.0	146	2	AAW22901	Aaw22901		Biology
8	736	100.0	146	2	AAW30791	Aaw30791		Obesity P
9	736	100.0	146	2	AAW26194	Aaw26194		Obesity P
10	736	100.0	146	2	AAW34483	Aaw34483		Human obe
11	736	100.0	146	2	AAW32575	Aaw32575		Anti obes
12	736	100.0	146	2	AAW34489	Aaw34489		Obesity P
13	736	100.0	146	2	AAW69682	Aaw69682		Human obe
14	736	100.0	146	2	AAW53342	Aaw53342		Obesity P
15	736	100.0	146	2	AAY43311	Aay43311		Human leptin
16	736	100.0	146	2	AAY06102	Aay06102		Human obe
17	736	100.0	146	3	AAY92712	Aay92712		Mature le
18	736	100.0	146	3	AAY81111	Aay81111		Mature hu
19	736	100.0	146	3	AAY80260	Aay80260		Human mat
20	736	100.0	146	3	AAV83768	Aav83768		Human OB
21	736	100.0	146	3	AAV97871	Aay97871		Mature wi
22	736	100.0	146	3	AAV95786	Aay95786		Mature re
23	736	100.0	146	3	AAV95531	Aay95531		Human mat
24	736	100.0	146	3	AAB14265	Aab14265		Mature hu
25	736	100.0	146	4	AAB070130	Aab070130		Mature hu

## ALIGNMENTS

RESULT 1		Location/Qualifiers	
ID	AAW00013	standard; protein;	146 AA.
XX			
AC	AAW00013;		
XX			
DT	30-SEP-1996	(first entry)	
XX			
DE	Acid stable modified ob protein	(Asp22Asn).	
XX			
KW	ob protein; adiposity regulating hormone; mouse; acid stability;		
KW	adsorption characteristic; obesity; type II diabetes;		
KW	cardiovascular disease; cancer.		
XX			
OS	Synthetic.		
XX			
PH			
FT	Misc-difference 22	/label= Asp22Asn	
FT	Disulfide-bond 96.	.146	
XX			
PN	EP725078-A1.		
XX			
XX			
PD	07-AUG-1996.		
XX			
PF	29-JAN-1996;	96EP-00300612.	
XX			
PR	31-JAN-1995;	95US-00381048.	
PR	06-FEB-1995;	95US-00383638.	
XX			
PA	(ELIL ) LILLY & CO ELI.		
XX			
PA	Basinsky MB, Dimarchi RD, Heath WF, Schonier BE,		
XX			
DR	WPI : 1996-356062/36.		
XX			
PT	Mammalian derived anti-obesity proteins which regulate fat tissue - used		
PT	for treating obesity and to reduce risk for type II diabetes,		
PT	cardiovascular disease and cancer.		
XX			
PS	This sequence represents a modified ob proteins. ob proteins are thought		
CC	to be adiposity regulating hormones. This sequence is based on the mouse		
CC	ob protein sequence. Proteins such as this have improved stability, esp.		
CC	acid stability, and improved adsorption characteristics compared to the		
CC	wild type protein disclosed in Yiyang Zhang et al., Nature 372: 425-32		
CC	(December 1994). These proteins correspond to the generic formulae Given		

CC in AAR9497-98). They are biologically active for the treatment of obesity. Individuals treated with these proteins have a reduced risk for type II diabetes, cardiovascular disease and cancer.

XX Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;

Best Local Similarity 100.0%; Pred. No. 7.8e-73; Mismatches 0; Indels 0; Gaps 0;

Matches 146; Conservative 0; Pred. No. 7.8e-73; Mismatches 0; Indels 0; Gaps 0;

Db 1 VPIQYQDDTKLTIKTVTRNDISHTQSISKQVTGGLDPIGHPILTLISKMDQTLLAV 60

Db 1 VPIQYQDDTKLTIKTVTRNDISHTQSISKQVTGGLDPIGHPILTLISKMDQTLLAV 60

Qy 61 YQQILTSMSRNLVQISNDLLENRLDLHVTAFSKSCHLPIWASGLTLDLGGVLEASGYS 120

Db 61 YQQILTSMSRNLVQISNDLLENRLDLHVTAFSKSCHLPIWASGLTLDLGGVLEASGYS 120

Qy 121 TEVVALSRQLGSQSLQDMILWQDLDLSPGC 146

Db 121 TEVVALSRQLGSQSLQDMILWQDLDLSPGC 146

#### RESULT 2

AAR9490 ID AAR9490 standard; protein; 146 AA.

XX AC AAR9490;

XX DT 16-OCT-2003 (revised)

XX DT 26-SEP-1996 (First entry)

DE Chimeric ob protein.

XX KW ob protein; human; substitution; murine; mouse; obesity; stability;

XX KW type II diabetes; cardiovascular disease; cancer.

OS Mus musculus.

OS Homo sapiens.

XX Chimeric.

#### Location/Qualifiers

PH Key Difference 22 /note= "Opt. Gln or Asp"

FT Misc-difference 27 /note= "Opt. Ala"

FT Misc-difference 28 /note= "Opt. Glu or absent"

FT Misc-difference 54 /note= "Opt. Ala"

FT Misc-difference 68 /note= "Opt. Leu"

FT Misc-difference 72 /note= "Opt. Glu or Asp"

FT Misc-difference 77 /note= "Opt. Ala"

FT Disulfide-bond 96 . 146

FT Misc-difference 97 /note= "Opt. replaced with Gln, Asn, Ala, Gly, Ser or Pro"

FT Misc-difference 100 /note= "Opt. replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"

FT Misc-difference 101 /note= "Opt. replaced with Ser, Asn, Gly, His, Pro, Thr or Val"

FT Misc-difference 102 /note= "Opt. replaced with Arg"

FT Misc-difference 103 /note= "Opt. replaced with Ala"

FT Misc-difference 105 /note= "Opt. replaced with Gln"

FT Misc-difference 106 /note= "Opt. replaced with Val"

FT Misc-difference 107 /note= "Opt. replaced with Lys or Ser"

FT Misc-difference 108 /note= "Opt. replaced with Pro"

FT Misc-difference 111 /note= "Opt. replaced with Glu"

FT Misc-difference 118 /note= "Opt. replaced with Asp"

FT Misc-difference 138 /note= "Opt. replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Gln"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Gln"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Gln"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Gln"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Gln"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Gln"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Gln"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Gln"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Gln"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

FT Misc-difference 146 /note= "Opt. replaced with Gln"

FT Misc-difference 146 /note= "Opt. replaced with Val or Leu"

XX /note= "Opt. replaced with Lys or Ser"

XX /note= "Opt. replaced with Pro"

XX /note= "Opt. replaced with Glu"

XX /note= "Opt. replaced with Asp"

</div

DT	13-SEB-1996	(first entry)	AAW30892	ID AAW30892 standard; protein; 146 AA.
XX	Human mature obesity protein.		XX	AAW30892;
DE			AC	AAW30892;
XX	Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;		XX	
KW	food intake; energy expenditure; high blood pressure; cholesterol; human;		DT	20-MAR-1998 (first entry)
KW	gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.		XX	
XX	Homo sapiens.		DE	Synthetic obesity protein.
OS			XX	
XX	Obesity protein; sucrose; trehalose; treatment; obesity; diabetes;		KW	
PN	GB2292382-A.		KW	cardiovascular disease; cancer.
XX			XX	
PD	21-FEB-1996.		OS	Synthetic.
XX			XX	
PF	17-AUG-1995;	95GB-00016947.	PN	EP797999-A2.
XX			XX	
PR	17-AUG-1994;	94US-00292345.	PD	01-OCT-1997.
PR	30-NOV-1994;	94US-00347563.	XX	
PR	01-MAY-1995;	95US-00438431.	PF	24-MAR-1997;
PR	07-JUN-1995;	95US-00483211.	XX	97EP-00301995.
XX			PR	26-MAR-1996;
PA	(UYRQ ) UNIV ROCKEFELLER.		PR	96US-0014177P.
XX			PR	05-APR-1996;
PI	Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;		XX	96US-0014951P.
PI	Burley SK;		XX	
XX			PA	(ELIL ) LILLY & CO ELI.
PS	WPI: 1996-090009/11.		PA	
XX	Obesity polypeptide(s) able to modulate body wt. - useful for e.g. reducing wt. in treatment of diabetes, high blood pressure and high cholesterol and for cosmetic reasons.		PI	Beals JM, Edwards MJ, Pikal MJ, Rinella JV,
XX			XX	
DR	DR		XX	
XX			DR	WPI; 1997-472913/44.
PT			XX	
PT			PT	Pharmaceutical compositions comprising obesity protein - and sucrose and/or trehalose.
PT			XX	
PS	Claim 11; Page ?; 304pp; English.		PS	Claim 2; Page 44; 48pp; English.
XX			XX	
CC	AAW00538-W00541 represent the mature proteins of the murine and human obesity polypeptides (OBP) (full length sequences represented by AAR92719 and AAR92720). OBP (also known as leptin) is a hormone involved in the regulation of body weight. This sequence has effects on both food intake and energy expenditure. OBP and its analogues are useful for modifying body weight (optionally combined with known medicaments), for treating diabetes, high blood pressure or high cholesterol. The DNA encoding this sequence (and sequences complimentary to it) can be used in gene therapy for modifying body weight. This protein is useful for reducing weight for health or cosmetic reasons in obese humans, or to produce leaner food animals. Antagonists of OBP (including antibodies) are useful for increasing body weight, e.g. for treating weight loss associated with cancer, or for cosmetic reasons in humans, or for production of Kobe beef or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in complex diagnostics for the presence of OBP. The formation of Ab-OBP complexes enables in vitro evaluation of levels of OBP in a sample, especially to detect diseases associated with elevated or decreased levels, and to monitor treatment of these diseases		CC	A novel pharmaceutical composition comprises an obesity protein, e.g. the present sequence, together with sucrose and/or trehalose. The composition can be used to treat obesity and associated disorders, e.g. diabetes, cardiovascular disease and cancer. The composition is stable and easy to manufacture
CC			XX	
CC			PS	Sequence 146 AA;
CC			XX	Query Match 100.0%; Score 736; DB 2; Length 146;
CC			CC	Best Local Similarity 100.0%; Pred. No. 7.8e-73; Mismatches 0; Indels 0; Gaps 0;
CC			CC	Macches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC			CC	1 VPIQKVQDDTKLIIKTVTRINDISHTQSVSQKVYGLDFIPGHPLTLSKMDTLAV 60
CC			Db	1 VPIQKVQDDTKLIIKTVTRINDISHTQSVSQKVYGLDFIPGHPLTLSKMDTLAV 60
CC			CC	61 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	61 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	62 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	62 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	63 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	63 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	64 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	64 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	65 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	65 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	66 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	66 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	67 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	67 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	68 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	68 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	69 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	69 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	70 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	70 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	71 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	71 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	72 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	72 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	73 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	73 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	74 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	74 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	75 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	75 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	76 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	76 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	77 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	77 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	78 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	78 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	79 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	79 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	80 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	80 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	81 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	81 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	82 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	82 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	83 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	83 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	84 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
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CC			CC	85 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	85 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	86 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	86 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	87 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	87 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	88 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	88 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	89 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	89 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	90 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	90 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	91 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	91 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	92 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	92 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	93 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	93 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	94 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	94 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	95 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	95 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	96 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	96 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	97 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	97 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	98 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	98 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	99 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	99 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	100 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	100 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	101 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	101 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	102 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	102 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	103 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	103 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	104 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	104 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	105 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	105 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	106 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	106 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	107 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	107 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	108 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	108 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	109 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	109 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	110 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	110 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	111 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	111 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	112 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	112 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	113 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	113 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	114 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	114 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	115 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	115 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	116 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	116 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	117 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	117 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	118 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	118 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	119 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	119 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	120 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			Db	120 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120
CC			CC	121 TEVVALSRQLQSLQMLWQLDLSPGC 146
CC			Db	121 TEVVALSRQLQSLQMLWQLDLSPGC 146
CC			CC	RESULT 5
Qy	1 VPIQKVQDDTKLIIKTVTRINDISHTQSVSQKVYGLDFIPGHPLTLSKMDTLAV 60		AAW34482;	
Db	1 VPIQKVQDDTKLIIKTVTRINDISHTQSVSQKVYGLDFIPGHPLTLSKMDTLAV 60		ID AAW34482.	
Qy	2 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120		AAW34482.	
Db	2 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120		XX	
Qy	3 YQQITSMPSMRNVIQISNDIENRLDILHVLAFSKSCHLPASGLETIDSLLGVLEASGYS 120		XX	
Db	3 YQQITSMPSMRNVIQ			



KW	Intermediate; recombinant; production; obesity; regulation; fatty tissue;	XX	12-MAR-1998 (first entry)
XX	treatment; disease; diabetes; cardiovascular; cancer; properly folded.	XX	Obesity protein complexed with a divalent metal cation.
OS	Mammalia.	XX	DB
XX		XX	Obesity protein complexed with a divalent metal cation.
Key Modified-site	Location/Qualifiers	XX	XX
PH	1	KW	Obesity protein; diabetes; cancer; cardiovascular disease;
FT	/label= Val-R3	KW	divalent metal cation; leader sequence.
FT	/note= "R3 is absent, Met, Met-R4 or leader sequence	XX	
FT	(preferably Met-Arg, Gly-Ser-Pro or 1 of AAW08589-94),	OS	Homo sapiens.
FT	and R4 is any amino acid other than Pro"	XX	
FT	96..146	FH	Location/Qualifiers
Disulfide-bond	WO9700886-A1.	Key Disulfide-bond	96..146
XX		XX	XX
PN		FT	FT
XX		W09728824-A1.	W09728824-A1.
PD	09-JAN-1997.	XX	PN
XX		PD	14-AUG-1997.
PP	20-JUN-1996;	XX	XX
XX	96WO-US010613.	PP	24-JAN-1997;
PR	22-JUN-1995;	XX	97WO-US001188.
XX	95US-0000451P.	PR	06-FEB-1996;
PA	(ELIL ) LILLY & CO ELI.	XX	96US-0011238P.
PA		PA	
PA	(ELIL ) LILLY & CO ELI.	XX	PA (ELIL ) LILLY & CO ELI.
PI		XX	
PI	Hale JE, Mackellar W;	PI	
XX		XX	Hoffmann JA;
DR	WPI; 1997-087317/08.	XX	
XX		DR	WPI; 1997-415077/38.
PT	Properly folded intermediate for obesity protein - prepd. from inclusion	XX	PT
PT	bodies, provides high yield of active protein for treatment of obesity	XX	PT
PT	and its complications.	XX	PT
PS	Claim 12; Page 21; 66pp; English.	XX	PT
XX		XX	PT
CC	AAW1015 is a properly folded intermediate for the production of the	XX	Claim 3; Page 26; 33pp; English.
CC	biologically active obesity protein AAW22901, which has a similar	XX	
CC	structure but comprises a disulphide bridge between Cys96 and Cys146.	XX	
CC	AAW1015 is the final intermediate in the renaturation of a recombinant	XX	
CC	protein to AAW22901, which is an active anti-obesity protein for the	XX	
CC	regulation of fatty tissue and treatment of obesity related diseases,	XX	
CC	e.g. diabetes, cardiovascular disease and cancer. The production of	XX	
CC	AAW22901 via AAW1015 provides a high yield of active protein, and	XX	
CC	permits large scale manufacture with a high concentration of protein	XX	
CC	during the folding stage. AAW1015 already has the correct tertiary	XX	
CC	structure and conversion to AAW22901 is almost quantitative, with minimal	XX	
CC	formation of S-S linked dimers or multimers, negating the need for an	XX	
CC	aggregation preventing agent. AAW1015 is stable in the presence or	XX	
CC	absence of denaturant, is soluble in phosphate buffered saline and can be	XX	
CC	purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)	XX	
SQ	Sequence 146 AA;	XX	
XX		XX	
Query Match	100..0%; Score 736; DB 2; Length 146;	XX	
Best Local Similarity	100..0%; Pred. No. 7..8e-73;	XX	
Matches 146; Conservative	0; Mismatches 0; Gaps 0;	XX	
Qy	1 VPIQRVQDDTKTLIKRTIVTRINDISHTQSVSOKVYGLDFIPGLHPILTSKMPDTLAV 60	Qy	1 VPIQKVQDDTKTLIKRTIVTRINDISHTQSVSOKVYGLDFIPGLHPILTSKMPDTLAV 60
Db	1 VPIQRVQDDTKTLIKRTIVTRINDISHTQSVSOKVYGLDFIPGLHPILTSKMPDTLAV 60	Db	1 VPIQKVQDDTKTLIKRTIVTRINDISHTQSVSOKVYGLDFIPGLHPILTSKMPDTLAV 60
Db	1 VPIQRVQDDTKTLIKRTIVTRINDISHTQSVSOKVYGLDFIPGLHPILTSKMPDTLAV 60	Db	1 VPIQRVQDDTKTLIKRTIVTRINDISHTQSVSOKVYGLDFIPGLHPILTSKMPDTLAV 60
Qy	61 YQQILTSMPSRNVIQISNDLENRLDILHVLAFSKSCHLPNSAGLETDLSGGVLEASGYS 120	Qy	61 YQQILTSMPSRNVIQISNDLENRLDILHVLAFSKSCHLPNSAGLETDLSGGVLEASGYS 120
Db	61 YQQILTSMPSRNVIQISNDLENRLDILHVLAFSKSCHLPNSAGLETDLSGGVLEASGYS 120	Db	61 YQQILTSMPSRNVIQISNDLENRLDILHVLAFSKSCHLPNSAGLETDLSGGVLEASGYS 120
Qy	121 TEVVALSRQLQGSQSLQDMWQLDLSPGC 146	Qy	121 TEVVALSRQLQGSQSLQDMWQLDLSPGC 146
Db	121 TEVVALSRQLQGSQSLQDMWQLDLSPGC 146	Db	121 TEVVALSRQLQGSQSLQDMWQLDLSPGC 146
RESULT 8	AAW30791 standard; protein; 146 AA.	RESULT 9	AAW26194 standard; protein; 146 AA.
ID	AAW30791	ID	AAW26194
XX		XX	
DE	Obesity protein analogue #6.	DE	Obesity protein analogue #6.
XX		XX	
KW	Obesity protein analogue; divalent metal cation complex; therapy; cancer;	XX	
KW	obesity; obesity associated disorder; diabetes; cardiovascular disease.	XX	
XX		OS	Synthetic.

XX	Location/Qualifiers	
PH	Disulfide-bond	96 . 146
FT	Misc-difference	97 . "optionally replaced with Gln, Asn, Ala, Gly, Ser or Pro"
FT	Misc-difference	100 /note= "optionally replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
FT	Misc-difference	101 /note= "optionally replaced with Ser, Asn, Gly, His, Pro, Thr or Val"
FT	Misc-difference	102 /note= "optionally replaced with Arg"
FT	Misc-difference	103 /note= "optionally replaced with Ala"
FT	Misc-difference	105 /note= "optionally replaced with Gln"
FT	Misc-difference	106 /note= "optionally replaced with Lys or Ser"
FT	Misc-difference	107 /note= "optionally replaced with Pro"
FT	Misc-difference	108 /note= "optionally replaced with Glu"
FT	Misc-difference	111 /note= "optionally replaced with Asp"
FT	Misc-difference	138 /note= "optionally replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
XX	W09726916-A1.	
XX	31-JUL-1997.	
XX	24-JAN-1997;	97WO-US001189.
PR	25-JAN-1996;	96US-0011055P.
XX	(ELIL ) LILLY & CO ELI.	
PI	Hoffmann JA;	
XX	WPI ; 1997-393377/36.	
DR		
XX	Obesity protein analogue complexed with divalent metal cation - useful for treating obesity and associated disorders, e.g. diabetes, cardiovascular disease and cancer.	
Disclosure;	Page 11; 45pp; English.	
PS	AAW26189, AAW26190 and AAW26192-W26201 represent obesity protein analogues contained in the compound of the invention. These sequences were synthetically created from the sequence shown in AAW26191. The compound of the invention comprises one of these obesity protein analogues complexed with a divalent metal cation (preferably Zn++). The specification does not indicate where the divalent metal cation complexes to on the obesity protein analogue. The compound of the invention (or a parenteral pharmaceutical formulation containing it) can be used to treat obesity. It may also be used to treat disorders associated with obesity such as diabetes, cardiovascular disease and cancer. The compound allows effective pharmaceutical treatment at lower doses that significantly reduce the risk of toxic or other undesirable effects. In addition, because the amount of protein administered is less, the cost of the unit dosage form to the patient is reduced	
XX	Sequence 146 AA;	
SQ	1 VPIQKQDDTKLTIKTVINDISHTQSOKVTLGDFIPGHPLTLSKMDQTLAY 60 YQQILTSMPSRNVIQISNDLENRLHLVAFSKSCLPWAISGLETDLSLGVLLEASGYS 61 YQQILTSMPSRNVIQISNDLENRLHLVAFSKSCLPWAISGLETDLSLGVLLEASGYS 61 YQQILTSMPSRNVIQISNDLENRLHLVAFSKSCLPWAISGLETDLSLGVLLEASGYS 120	
Db	1 VPIQKQDDTKLTIKTVINDISHTQSOKVTLGDFIPGHPLTLSKMDQTLAY 60 YQQILTSMPSRNVIQISNDLENRLHLVAFSKSCLPWAISGLETDLSLGVLLEASGYS 61 YQQILTSMPSRNVIQISNDLENRLHLVAFSKSCLPWAISGLETDLSLGVLLEASGYS 61 YQQILTSMPSRNVIQISNDLENRLHLVAFSKSCLPWAISGLETDLSLGVLLEASGYS 120	
QY	121 TEVVALSRQLGSQMLWOLDLSPGC 146 YQQILTSMPSRNVIQISNDLENRLHLVAFSKSCLPWAISGLETDLSLGVLLEASGYS 121 TEVVALSRQLGSQMLWOLDLSPGC 146	
Db	121 TEVVALSRQLGSQMLWOLDLSPGC 146 YQQILTSMPSRNVIQISNDLENRLHLVAFSKSCLPWAISGLETDLSLGVLLEASGYS 121 TEVVALSRQLGSQMLWOLDLSPGC 146	

AAW32575	61 YQQILTSMPRSNVIQISNDLENLRLDHLVLAFLSKSCHLPWASGLTLDLSICGVLEASGYS 120
ID AAW32575 standard; protein; 146 AA.	
XX	
AC AAW32575;	
XX	
DT 22-JAN-1998 (first entry)	
XX	
DB Anti obesity protein analogue.	
XX	
KW Anti obesity protein analogue; neuropeptide Y; radiovascular; renal;	
KW cerebral; central nervous system; CNS; heart; blood vessel;	
KW sympathetic nerve; mouse; human; pain; nociception;	
KW abnormal gastrointestinal motility; secretion;	
KW abnormal drink intake disorder; abnormal food intake disorder;	
KW sexual dysfunction; reproductive disorder; obesity.	
XX	
OS Homo sapiens.	
OS Synthetic.	
XX	
FH Key Disulfide-bond 96 . 146	Location/Qualifiers
XX EP759441-A2.	
PN	
XX 26-FEB-1997.	
PD XX	
PF 26-JUN-1996; 96EP-00304723.	
XX	
PR 30-JUN-1995; 95US-0000740P.	
PR 30-JUN-1995; 95US-0000752P.	
PR 27-OCT-1995; 95US-0005910P.	
PR 27-OCT-1995; 95US-0005911P.	
XX	
PA (ELIL ) LILLY & CO EU.	
PI Bue-Valleskey JM, Heiman ML, Stephens TW, Tinsley FC;	
XX	
DR WPI; 1997-147497/14.	
XX	
PT New use of biologically active anti-obesity protein analogues - for	
PT treating conditions associated with excess neuropeptide Y, e.g.	
PT cardiovascular, renal, cerebral or CNS disorders.	
XX	
PS Claim 8; Page 84; 89pp; English.	
XX	
CC The present sequence represents an anti obesity protein analogue used in	
CC the treatment or prevention of a condition associated with an excess of	
CC neuropeptide Y. The protein analogue is useful in the treatment or	
CC prevention of disorders or diseases pertaining to the heart, blood	
CC vessels or the renal system, conditions related to increased sympathetic	
CC nerve activity, cerebral diseases and diseases related to the central	
CC nervous system, conditions related to pain or nociception, diseases	
CC related to abnormal gastrointestinal motility and secretion, abnormal	
CC drink and food intake disorders, diseases related to sexual dysfunction	
CC and reproductive disorders, and conditions or disorders associated with	
CC obesity. The protein analogue has improved properties due to its lower	
CC isolectric point and due to specific substitutions to the human obesity	
CC protein. It is more stable than both the mouse and human obesity protein,	
CC and is therefore superior therapeutic agents. It is more readily	
CC formulated and stored.	
XX	
SQ Sequence 146 AA;	
DR 100.0% ; Score 736; DB 2; Length 146;	
Best Local Similarity 100.0% ; Pred. No. 7.8e-73;	
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB 1 VPIQKVDPDTKLTKITIVTRINDISHTQSVSSKQVTKDGFPGLHPLTLSKMDTTLAV 60	
1 VPQKVDPDTKLTKITIVTRINDISHTQSVSSKQVTKDGFPGLHPLTLSKMDTTLAV 60	
Qy 61 YQQILTSMPRSNVIQISNDLENLRLDHLVLAFLSKSCHLPWASGLTLDLSIGYLEASGYS 120	
XX	
Query Match	New obesity protein analogue compositions - comprising a soluble
Best Local Similarity	parenteral formulation containing a preservative selected from an
Matches 146;	alkyl:paraben and chloro:butanol.
DB	Disclosure; Page 10; 46pp; English.
Qy	XX This sequence represents an obesity protein analogue, and can be used in
CC the formulation of the invention. The formulation of the invention is a	CC soluble parenteral formulation that comprises an obesity protein analogue

CC and a preservative selected from an alkylparaben, chlorobutanol, or a mixture. The compositions can be used for the treatment of obesity and disorders associated with obesity. In the formulations, the obesity protein analogue remains stable and soluble at much higher concentrations and at a pH range acceptable for a soluble, multi-use parenteral formulation.

## Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;  
Best Local Similarity 100.0%; Pred. No. 7.8e-73;  
Matches 146; Conservative 0; Mismatches 0; Gaps 0;  
SQ Sequence 146 AA;

```

Qy   1 VPIQKVQDDTKLTIKTTVTRINDISHTQSVSSSKQKVTKGLDFPGLAHLITLSKMDTLAV 60
Db   1 VPIQKVQDDTKLTIKTTVTRINDISHTQSVSSSKQKVTKGLDFPGLAHLITLSKMDTLAV 60
Qy   61 YQQILTSMPNSRNVIQSNDLNLRLDILHVLIAFSKSCHLPWASGLETLDSLGCVLAEASGYS 120
Db   61 YQQILTSMPNSRNVIQSNDLNLRLDILHVLIAFSKSCHLPWASGLETLDSLGCVLAEASGYS 120
Qy   121 TEVVALSRLOGSLQDMWQLDLSPGC 146
Db   121 TEVVALSRLOGSLQDMWQLDLSPGC 146
Qy   121 TEVVALSRLOGSLQDMWQLDLSPGC 146
Db   121 TEVVALSRLOGSLQDMWQLDLSPGC 146

```

## RESULT 14

ID AAW69612 Standard; protein; 146 AA.

XX

AC AAW69612;

XX

DT 07-DEC-1998 (First entry)

XX

DE Human obesity protein.

XX

KW Obesity protein; therapy; human.

XX

Homo sapiens.

OS

PN WO9831391-A1.

XX

PD 23-JUL-1998.

XX

PR 16-JAN-1998;

XX

PR 17-JAN-1997;

XX

PR 07-AUG-1997;

XX

PA (ELIL ) LILLY &amp; CO ELI.

PI Rinella JV;

XX

DR WPI: 1998-413818/35.

XX

PT Obesity protein soluble formulation for treating obesity - has pH greater than 8.0, at which aggregation of obesity proteins by preservatives is reduced, allowing production of multi-use formulation.

PS Disclosure; Page 11-12; 30pp; English.

XX

CC This is the amino acid sequence of human obesity protein. The invention discloses a storage-stable, soluble formulation comprising an obesity protein and a preservative, and having a pH greater than 8.0. The obesity protein used in the formulation is preferably bio-synthesised in a host cell transformed with a recombinant DNA comprising a synthetic or semi-synthetic DNA encoding tge protein. The soluble formulation can be administered to mammals to treat obesity (claimed), especially humans when the obesity protein is human obesity protein. It was found that the physical stability of obesity proteins in the presence of preservatives such as phenol and cresol changes abruptly and is greatly enhanced at pH values above 8.0, such that the aggregation of obesity proteins caused by preservatives is reduced. At pH above 8.0, obesity proteins remain in

CC solution in the presence of certain preservatives, making possible a multi-use parenteral formulation containing those preservatives

XX SQ Sequence 146 AA;

Query Match	Score 736; DB 2; Length 146;
Best Local Similarity	100.0%; Pred. No. 7.8e-73;
Matches	146; Conservative 0; Mismatches 0; Gaps 0;
Sequence	146 AA;

Query	1 VPIQKVQDDTKLTIKTTVTRINDISHTQSVSSSKQKVTKGLDFPGLAHLITLSKMDTLAV 60
Db	1 VPIQKVQDDTKLTIKTTVTRINDISHTQSVSSSKQKVTKGLDFPGLAHLITLSKMDTLAV 60
Qy	61 YQQILTSMPNSRNVIQSNDLNLRLDILHVLIAFSKSCHLPWASGLETLDSLGCVLAEASGYS 120
Db	61 YQQILTSMPNSRNVIQSNDLNLRLDILHVLIAFSKSCHLPWASGLETLDSLGCVLAEASGYS 120
Qy	61 YQQILTSMPNSRNVIQSNDLNLRLDILHVLIAFSKSCHLPWASGLETLDSLGCVLAEASGYS 120
Db	61 YQQILTSMPNSRNVIQSNDLNLRLDILHVLIAFSKSCHLPWASGLETLDSLGCVLAEASGYS 120
Qy	121 TEVVALSRLOGSLQDMWQLDLSPGC 146
Db	121 TEVVALSRLOGSLQDMWQLDLSPGC 146

RESULT 14

ID	AAW53342 Standard; protein; 146 AA.
XX	XX
AC	AAW53342;
XX	XX
XX	20-JUL-1998 (First entry)
DB	Obesity protein analogue formula I I SEQ ID NO:4.
XX	XX
KW	Human; obesity protein; soluble; parenteral formulation; anionic; amphiphilic; ob gene; ob protein.
XX	XX
OS	Synthetic.
XX	XX
FH	Location/Qualifiers
FT	Key
FT	Misc-difference 97
FT	/note= "His can be replaced with Gln, Asn, Ala, Gly, Ser, or Pro"
FT	Misc-difference 100
FT	/note= "Trp can be replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu"
FT	Misc-difference 101
FT	/note= "Ala can be replaced with Ser, Asn, Gly, His, Pro, Thr, Val"
FT	Misc-difference 102
FT	/note= "Ser can be replaced with Arg"
FT	Misc-difference 103
FT	/note= "Gly can be replaced with Ala"
FT	Misc-difference 105
FT	/note= "Glu can be replaced with Gln"
FT	Misc-difference 106
FT	/note= "Thr can be replaced with Lys or Ser"
FT	Misc-difference 107
FT	/note= "Leu can be replaced with Pro"
FT	Misc-difference 108
FT	/note= "Asp can be replaced with Glu"
FT	Misc-difference 111
FT	/note= "Gly can be replaced with Asp"
FT	Misc-difference 138
FT	/note= "Trp can be replaced with Ala, Glu, Val, or Leu; or a Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu; or a pharmaceutically acceptable salt thereof"
PN	EP827750-A2.
XX	XX
PD	11-MAR-1998.
XX	XX
PF	97EP-00306420.
XX	XX
PF	22-AUG-1997;
XX	XX
PF	96US-0024121P.
PR	23-AUG-1996;

PR 23-AUG-1996; 96US-0025207P.  
 XX (ELIL ) LILLY & CO BLI.  
 PI Beals JM, Rinella JV;  
 XX WPI; 1998-180894/17.  
 XX PT Parenteral obesity protein formulations - containing anionic amphiphilic  
 PT stabiliser and stabilise.  
 PS Disclosure; Page 9; 45pp; English.  
 XX The present sequence represents an obesity protein generic formula for  
 CC producing obesity protein analogues for use in the present invention as  
 CC part of a soluble parenteral formulation. The soluble parenteral  
 CC formulations comprises an obesity protein or obesity protein analogue and  
 CC an anionic amphiphilic compound. The formulations are used for treating  
 CC obesity and associated disorders. The proteins are preferably present at  
 CC a concentration of 5-50 mg/ml. The anionic amphiphilic compound  
 CC solubilises and stabilises the protein  
 XX Sequence 146 AA;  
 SQ Query Match 100.0%; Score 736; DB 2; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-73;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 VPIQKVQDDDTKLTKITVTRINDISHTQSYSKQVTGLDFIPGLPILTSKMDQTLLAV 60  
 1 VPIQKVQDDDTKLTKITVTRINDISHTQSYSKQVTGLDFIPGLPILTSKMDQTLLAV 60  
 Qy 61 YQQILTSMPSRNVIQISNDLNRDILHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120  
 Db 61 YQQILTSMPSRNVIQISNDLNRDILHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120  
 Qy 121 TEVVVALSRQLQSLQDMWQLDLSPGC 146  
 Db 121 TEVVVALSRQLQSLQDMWQLDLSPGC 146  
 Qy 121 TEVVVALSRQLQSLQDMWQLDLSPGC 146  
 Db 121 TEVVVALSRQLQSLQDMWQLDLSPGC 146

Search completed: March 12, 2005, 04:59:56  
 Job time : 118.15 secs

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RESULT 15  
 AAY43311  
 ID AAY43311 standard; protein; 146 AA.  
 XX AC AAY43311;  
 XX DT 21-JAN-2000 (first entry)  
 DE Human leptin.  
 XX Leptin; brain function improver; brain denaturation disease; therapy;  
 KW Alzheimer's disease; old age dementia; Pick's disease;  
 KW hereditary aphasia; Huntington's chorea; Parkinson's disease;  
 KW progressive subcutaneous gliosis; progressive supranuclear paralysis;  
 KW thalamus denaturation; myoclonus epilepsy.  
 OS Homo sapiens.  
 XX PN JP11279074-A.  
 XX PD 12-OCT-1999.  
 XX PF 26-MAR-1998; 98JP-00100202.  
 XX PR 26-MAR-1998; 98JP-00100202.  
 PA (OMUR/) OMURA H.  
 PA (HORI/) HORI N.  
 PA (SHIR/) SHIRASHI T.  
 PA (SASA/) SASAKI K.  
 PA (TAKE/) TAKEDA H.  
 PA (TSUJ/) TSUJI M.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:53:33 ; Search time 28 4537 Seconds  
(without alignments)  
383.035 Million cell updates/sec

Title: US-10-049-182-6  
Perfect score: 736  
Sequence: 1 VP1QKVQDDTKTLLIKTIVTR.....SRLQGSILQDMLWQLDLSPGC 146

Scoring table: BLOSSM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 4 summaries

Database : Issued Patents AA:  
1: /cgns\_6/podata/1/iaa/5A\_COMB.pep:  
2: /cgns\_6/podata/1/iaa/5B\_COMB.pep:  
3: /cgns\_6/podata/1/iaa/6A\_COMB.pep:  
4: /cgns\_6/podata/1/iaa/6B\_COMB.pep:  
5: /cgns\_6/podata/1/iaa/PCUTUS\_COMB.pep:  
6: /cgns\_6/podata/1/iaa/backfiles1.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the core of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	146	1 US-08-398-021-3	Sequence 3, Appli
2	736	100.0	146	2 US-08-388-943A-5	Sequence 5, Appli
3	736	100.0	146	2 US-08-623-104-3	Sequence 3, Appli
4	736	100.0	146	2 US-09-003-001-6	Sequence 6, Appli
5	736	100.0	146	3 US-08-648-262-6	Sequence 6, Appli
6	736	100.0	146	3 US-08-648-262-6	Sequence 6, Appli
7	736	100.0	146	3 US-08-914-375C-32	Sequence 32, Appli
8	736	100.0	146	4 US-09-172-644-1	Sequence 1, Appli
9	736	100.0	146	4 US-09-221-178-1	Sequence 1, Appli
10	736	100.0	146	4 US-09-200-919-1	Sequence 1, Appli
11	736	100.0	146	5 PCT-US26-00952-2	Sequence 2, Appli
12	736	100.0	146	5 PCT-US26-00952-3	Sequence 3, Appli
13	736	100.0	147	4 US-09-200-919-4	Sequence 4, Appli
14	736	100.0	148	1 US-08-429-362-3	Sequence 3, Appli
15	736	100.0	148	2 US-08-833-104-18	Sequence 18, Appli
16	736	100.0	167	2 US-08-540-242A-4	Sequence 4, Appli
17	736	100.0	167	2 US-08-347-563A-4	Sequence 4, Appli
18	736	100.0	167	2 US-09-003-081-5	Sequence 5, Appli
19	736	100.0	167	3 US-08-392-345B-4	Sequence 4, Appli
20	736	100.0	167	3 US-08-648-262-5	Sequence 5, Appli
21	736	100.0	167	3 US-08-648-265-5	Sequence 4, Appli
22	736	100.0	167	3 US-08-685-902A-4	Sequence 4, Appli
23	736	100.0	167	3 US-08-188-214A-4	Sequence 4, Appli
24	736	100.0	167	3 US-08-488-208A-4	Sequence 4, Appli
25	736	100.0	167	3 US-08-599-628-1	Sequence 1, Appli
26	736	100.0	167	3 US-08-988-908-7	Sequence 7, Appli
27	736	100.0	167	3 US-08-483-211A-4	Sequence 4, Appli

## ALIGNMENTS

RESULT 1  
US-08-398-021-3  
; Sequence 3, Application US/08398021  
; Patent No. 5594101  
; GENERAL INFORMATION:  
; APPLICANT: Becker, Gerald W.  
; APPLICANT: Hale, John E.  
; APPLICANT: Mackellar L., Warren C.  
; TITLE OF INVENTION: ANTI-OBESEITY PROTEINS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center/Patent Division  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: United States  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/398-021  
; APPLICATION NUMBER: US/08/398-021  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Caltrider, Steven P.  
; REGISTRATION NUMBER: 36,467  
; REFERENCE/DOCKET NUMBER: X10001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 317-276-0575  
; TELEFAX: 317-277-1917  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 146 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-398-021-3

Query Match 100.0%; Score 736; DB 1; Length 146;  
Best Local Similarity 100.0%; Pred. No. 4e-74;  
Matches 146; Conservative 0; Gaps 0;  
Qy 1 VPIQRQDDTKLKLITVTRINDISHTQSNSKQRTGLDTPGIPILTSKMDQTFLAV 60  
Db 1 VPIQRQDDTKLKLITVTRINDISHTQSNSKQRTGLDTPGIPILTSKMDQTFLAV 60

RESULT 2  
 Qy 61 YQQILTMSRNVIQISNDLENLRLILHVAFLSKSCHLPPWASGLTLDSLGGVLEASGYS 120  
 Db 61 YQQILTMSRNVIQISNDLENLRLILHVAFLSKSCHLPPWASGLTLDSLGGVLEASGYS 120  
 Qy 121 TEVVALSRLOSSLDQMLWLQDLSPGC 146  
 Db 121 TEVVALSRLOSSLDQMLWLQDLSPGC 146

APPLICANT: Foster, Lisa K  
 APPLICANT: Furman, Thomas C  
 APPLICANT: MacKellar, Warren C  
 TITLE OF INVENTION: Process for Preparing Obesity Protein  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Eli Lilly & Company  
 STREET: Lilly Corporate Center  
 CITY: Indianapolis  
 STATE: Indiana  
 COUNTRY: USA  
 ZIP: 46285  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/823.104  
 FILING DATE: 24-MAR-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/429,362  
 FILING DATE: 26-APR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Caltrider, Steven P  
 REGISTRATION NUMBER: 36467  
 REFERENCE/DOCKET NUMBER: 10022A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 317-277-8110  
 TELEFAX: 317-277-1917  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 146 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 77  
 OTHER INFORMATION: /note= "Ser at position 77 is replaced with Ala"  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 97  
 OTHER INFORMATION: /note= "His at position 97 is replaced with Gln, Asn, Ala, Glu, Ser, or Pro"  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 100  
 OTHER INFORMATION: /note= "Trp at position 100 is replaced with Ala, Glu, Asp, Asn, Met, Ser, Thr, or Gly"  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 101  
 OTHER INFORMATION: /note= "Ala at position 101 is replaced with Ser, Asn, Glu, His, Pro, Thr, or Val"  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 102  
 OTHER INFORMATION: /note= "Ser at position 102 is replaced with Arg"  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 103  
 OTHER INFORMATION: /note= "Gly at position 103 is replaced with Ala"  
 FEATURE:

RESULT 3  
 US-08-823-104-3  
 Sequence 3, Application US/08823104  
 Patent No. 5840517  
 GENERAL INFORMATION:  
 APPLICANT: Atkinson, Paul R



INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

US-08-648-263-6

Query Match Score 736; DB 3; Length 146;  
Best Local Similarity 100.0%; Pred. No. 4e-74;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKLTKITIVTRINDISHTQSVSSKQKVTLGDLFIPGHPILTLSKMDQTAV 60  
Db 1 VPIQKVQDDTKLTKITIVTRINDISHTQSVSSKQKVTLGDLFIPGHPILTLSKMDQTAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENRLDILHVAFSKSCHLPWASGLETLDSLGGLVEASGYS 120  
Db 61 YQQILTSMPSRNVIQISNDLENRLDILHVAFSKSCHLPWASGLETLDSLGGLVEASGYS 120

Qy 1 VPIQKVQDDTKLTKITIVTRINDISHTQSVSSKQKVTLGDLFIPGHPILTLSKMDQTAV 60  
Db 1 VPIQKVQDDTKLTKITIVTRINDISHTQSVSSKQKVTLGDLFIPGHPILTLSKMDQTAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENRLDILHVAFSKSCHLPWASGLETLDSLGGLVEASGYS 120  
Db 61 YQQILTSMPSRNVIQISNDLENRLDILHVAFSKSCHLPWASGLETLDSLGGLVEASGYS 120

RESULT 7  
US-08-914-375C-32

Sequence 32, Application US/08914375C  
Patient No. 637783

GENERAL INFORMATION:  
APPLICANT: Steven A. Benner  
APPLICATION NUMBER: US/08/914,375C  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
APPLICANT: Steven A. Benner  
STREET: 1501 NW 68th Terrace  
CITY: Gainesville  
STATE: FL  
ZIP: 32605-4147  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: Apple Macintosh 7.0  
OPERATING SYSTEM: Macintosh 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/914,375C  
FILING DATE: 19-Aug-1997  
CLASSIFICATION: 702/20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-392-7773  
TELEFAX: 352-331-0462  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: amino acid  
ORIGINAL SOURCE:  
ORGANISM: human  
FEATURE:  
OTHER INFORMATION: leptin

US-08-914-375C-32

Sequence Description: SEQ ID NO: 32:

Query Match Score 736; DB 3; Length 146;  
Best Local Similarity 100.0%; Pred. No. 4e-74;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKLTKITIVTRINDISHTQSVSSKQKVTLGDLFIPGHPILTLSKMDQTAV 60  
Db 1 VPIQKVQDDTKLTKITIVTRINDISHTQSVSSKQKVTLGDLFIPGHPILTLSKMDQTAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENRLDILHVAFSKSCHLPWASGLETLDSLGGLVEASGYS 120  
Db 61 YQQILTSMPSRNVIQISNDLENRLDILHVAFSKSCHLPWASGLETLDSLGGLVEASGYS 120

**RESULT 8**  
US-09-172-644-1  
Sequence 1, Application US/09172644  
Patent No. 6,120,339;  
GENERAL INFORMATION:  
APPLICANT: GEGG, COLIN  
TITLE OF INVENTION: SITE-DIRECTED DUAL PEGYLATION OF PROTEINS FOR IMPROVED  
TITLE OF INVENTION: BIOACTIVITY AND BIOCOMPATIBILITY  
FILE REFERENCE: A-567  
CURRENT APPLICATION NUMBER: US/09/172,644  
CURRENT FILING DATE: 1998-10-14  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 146  
TYPE: PRT  
ORGANISM: Human Leptin

US-09-172-644-1

Query Match 100.0%; Score 736; DB 4; Length 146;  
Best Local Similarity 100.0%; Pred. No. 4e-74; Mismatches 0; Indels 0; Gaps 0;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKLTKITVTRINDIISHTQSVSQSKQVTGLDFPGLHPILTLSKMDQTAV 60  
Db 1 VPIQKVQDDTKLTKITVTRINDIISHTQSVSQSKQVTGLDFPGLHPILTLSKMDQTAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120  
Db 61 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

Qy 121 TEVVALSRQLQSLQDMWQLDLSPGC 146  
Db 121 TEVVALSRQLQSLQDMWQLDLSPGC 146

**RESULT 9**  
US-09-221-178-1  
Sequence 1, Application US/09221178  
Patent No. 6,451,346;  
GENERAL INFORMATION:  
APPLICANT: SHAH, SUBODH  
TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL FOR  
TITLE OF INVENTION: SUSTAINED DELIVERY OF BIOLOGICALLY ACTIVE AGENTS  
FILE REFERENCE: A-575  
CURRENT APPLICATION NUMBER: US/09/221,178  
CURRENT FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 146  
TYPE: PRT  
ORGANISM: Human Leptin

US-09-221-178-1

Query Match 100.0%; Score 736; DB 4; Length 146;  
Best Local Similarity 100.0%; Pred. No. 4e-74; Mismatches 0; Indels 0; Gaps 0;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKLTKITVTRINDIISHTQSVSQSKQVTGLDFPGLHPILTLSKMDQTAV 60  
Db 1 VPIQKVQDDTKLTKITVTRINDIISHTQSVSQSKQVTGLDFPGLHPILTLSKMDQTAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

Query Match      100.0%;    Score 736;    DB 5;    Length 146;  
 Best Local Similarity    100.0%;    Pred. No. 4e-74;  
 Matches 146;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 ; CURRENT APPLICATION NUMBER: US/09/200,919  
 ; CURRENT FILING DATE: 1998-11-30  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 147  
 ; TYPE: PRT  
 ; ORGANISM: HUMAN  
 ; US-09-200-919-4

Qy 1 VPIQKQDDTKLTKITVTRINDISHTQSVSQSKVTVGDFIPGLHPILTSKMDQTAV 60  
 Db 1 VPIQKQDDTKLTKITVTRINDISHTQSVSQSKVTVGDFIPGLHPILTSKMDQTAV 60  
 ; Query Match      100.0%;    Score 736;    DB 4;    Length 147;  
 Best Local Similarity    100.0%;    Pred. No. 4.e-74;  
 Matches 146;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 ; Query Match      100.0%;    Score 736;    DB 4;    Length 147;  
 Best Local Similarity    100.0%;    Pred. No. 4.e-74;  
 Matches 146;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 ; Query Match      100.0%;    Score 736;    DB 4;    Length 147;  
 Best Local Similarity    100.0%;    Pred. No. 4.e-74;  
 Matches 146;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;

Qy 61 YQQILTSMPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSIGGVLEASGS 120  
 Db 61 YQQILTSMPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSIGGVLEASGS 120  
 ; RESULT 12  
 PCT-US96-00952-3  
 ; Sequence 3, Application PC/TUS9600952  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: Anti-Obesity Proteins  
 ; NUMBER OF SEQUENCES: 16  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US96/00952  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 146 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: protein  
 PCT-US96-00952-3

Query Match      100.0%;    Score 736;    DB 5;    Length 146;  
 Best Local Similarity    100.0%;    Pred. No. 4e-74;  
 Matches 146;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 ; Query Match      100.0%;    Score 736;    DB 5;    Length 146;  
 Best Local Similarity    100.0%;    Pred. No. 4e-74;  
 Matches 146;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 ; Query Match      100.0%;    Score 736;    DB 5;    Length 146;  
 Best Local Similarity    100.0%;    Pred. No. 4e-74;  
 Matches 146;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;

Qy 1 VPIQKQDDTKLTKITVTRINDISHTQSVSQSKVTVGDFIPGLHPILTSKMDQTAV 60  
 Db 1 VPIQKQDDTKLTKITVTRINDISHTQSVSQSKVTVGDFIPGLHPILTSKMDQTAV 60  
 ; Query Match      100.0%;    Score 736;    DB 4;    Length 146;  
 Best Local Similarity    100.0%;    Pred. No. 4.e-74;  
 Matches 146;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;  
 ; Query Match      100.0%;    Score 736;    DB 4;    Length 146;  
 Best Local Similarity    100.0%;    Pred. No. 4.e-74;  
 Matches 146;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;

Qy 61 YQQILTSMPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSIGGVLEASGS 120  
 Db 61 YQQILTSMPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSIGGVLEASGS 120  
 ; RESULT 13  
 US-09-200-919-4  
 ; Sequence 4, Application US/09200919  
 ; GENERAL INFORMATION:  
 ; PATENT NO.: 5518235  
 ; APPLICANT: COMURA, YUTAKA  
 ; APPLICANT: HORI, NORIKI  
 ; APPLICANT: SHIRAIishi, TAKENASA  
 ; APPLICANT: SASAKI, KAZUO  
 ; APPLICANT: TAKEDA, HIROSHI  
 ; APPLICANT: TSUJI, MINORU  
 ; APPLICANT: MATSUMIYA, TERUHIKO  
 ; TITLE OF INVENTION: DRUG FOR IMPROVEMENT OF BRAIN FUNCTION  
 ; FILE REFERENCE: YAMA-100

Qy 1 VPIQKQDDTKLTKITVTRINDISHTQSVSQSKVTVGDFIPGLHPILTSKMDQTAV 60

RESULT 15  
 US-08-823-104-18  
 Sequence 18, Application US/08823104  
 Patent No. 5940517

GENERAL INFORMATION:  
 APPLICANT: Atkinson, Paul R  
 APPLICANT: Foster, Lisa K  
 APPLICANT: Furman, Thomas C  
 APPLICANT: Mackellar, Warren C  
 TITLE OF INVENTION: Process for Preparing Obesity Protein  
 NUMBER OF SEQUENCES: 18  
 ADDRESS: Eli Lilly & Company  
 STREET: Lilly Corporate Center  
 CITY: Indianapolis  
 STATE: Indiana  
 COUNTRY: USA  
 ZIP: 46285

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/823,104  
 FILING DATE: 24-MAR-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/429,362  
 FILING DATE: 16-APR-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Caltrider, Steven P  
 REGISTRATION NUMBER: 36467  
 REFERENCE/DOCKET NUMBER: 10022A

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 317-277-8110  
 TELEFAX: 317-277-1917

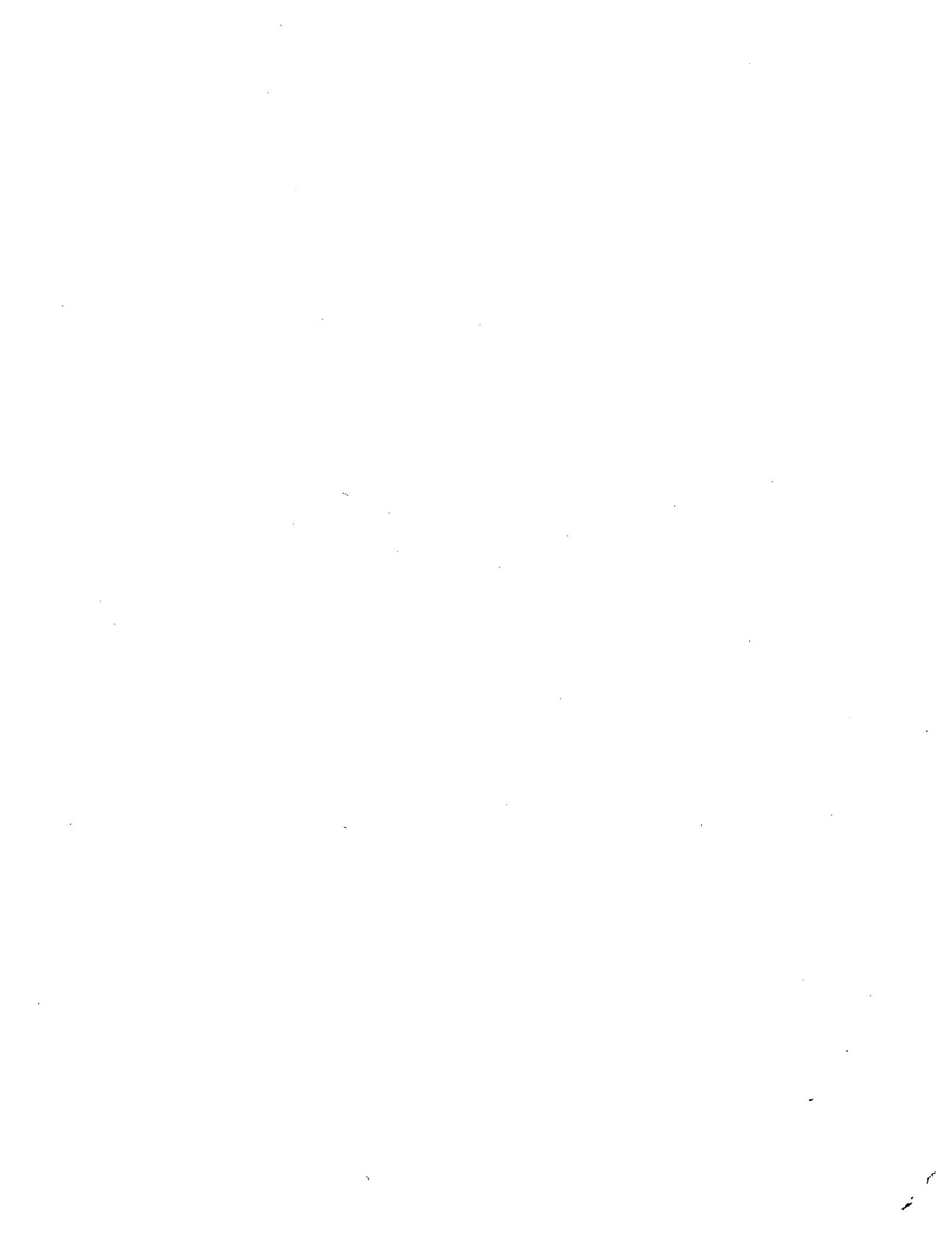
INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 148 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal

US-08-823-104-18

Query Match 100 0%; Score 736; DB 2; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDPTKTLIKITVTRINDIQTISQVSQKQVTKLDPFGHPILTLSKMDQTLLAV 60  
 Db 3 VPIQKVDPTKTLIKITVTRINDIQTISQVSQKQVTKLDPFGHPILTLSKMDQTLLAV 62

Qy 61 YQQILTSMPSRNVIQISNDLENLRDLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120  
 Db 63 YQQILTSMPSRNVIQISNDLENLRDLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 122



GenCore version 5.1.6									
Copyright (c) 1993 - 2005 Compugen Ltd.									
1 Protein - protein search, using SW model									
Run on: March 12, 2005, 05:03:46 ; Search time: 82.0958 seconds									
(without alignments)									
586.599 Million cell updates/sec									
Title: US-10-049-182-6									
Search score: 736									
Scoring table: BLOSUM62									
Gap open: 10.0 , Gapext: 0.5									
Searched: 1396920 seqs, 329844838 residues									
Total number of hits satisfying chosen parameters:									
1396920									
Minimum DB seq length: 0									
Maximum DB seq length: 2000000000									
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
Database :									
1:	/cgn2_6/ptodata/1/pubpaas/pct/us07_pubcomb.pep:*								
2:	/cgn2_6/ptodata/1/pubpaas/pct/new_pub_pep:*								
3:	/cgn2_6/ptodata/1/pubpaas/us06_new_pub_pep:*								
4:	/cgn2_6/ptodata/1/pubpaas/us16_pubcomb.pep:*								
5:	/cgn2_6/ptodata/1/pubpaas/us16_new_pub_pep:*								
6:	/cgn2_6/ptodata/1/pubpaas/pct/us07_pubcomb.pep:*								
7:	/cgn2_6/ptodata/1/pubpaas/us08_new_pub_pep:*								
8:	/cgn2_6/ptodata/1/pubpaas/us08_pubcomb.pep:*								
9:	/cgn2_6/ptodata/1/pubpaas/us09_pubcomb.pep:*								
10:	/cgn2_6/ptodata/1/pubpaas/us09_pubcomb.pep:*								
11:	/cgn2_6/ptodata/1/pubpaas/us10_pubcomb.pep:*								
12:	/cgn2_6/ptodata/1/pubpaas/us10_pubnew_pub_pep:*								
13:	/cgn2_6/ptodata/1/pubpaas/us10_pubnew_pub_pep:*								
14:	/cgn2_6/ptodata/1/pubpaas/us10b_pubcomb.pep:*								
15:	/cgn2_6/ptodata/1/pubpaas/us10c_pubcomb.pep:*								
16:	/cgn2_6/ptodata/1/pubpaas/us10d_pubcomb.pep:*								
17:	/cgn2_6/ptodata/1/pubpaas/us11_new_pub_pep:*								
18:	/cgn2_6/ptodata/1/pubpaas/us11_new_pub_pep:*								
19:	/cgn2_6/ptodata/1/pubpaas/us60_new_pub_pep:*								
20:	/cgn2_6/ptodata/1/pubpaas/us60_pubcomb.pep:*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									

RESULT 2  
US-10-139-794-10  
; Sequence 10, Application US/10139794  
; GENERAL INFORMATION:  
; APPLICANT: HYBRIDENICS, LYNX THERAPEUTICS INC.  
; APPLICANT: Pierre Legrain, Simon Whiteside, Jen-I Mao, Irina Khrebtukova, Shujun Lu  
; TITLE OF INVENTION: Protein-Protein Interactions In Adipocyte Cells (3)  
; FILE REFERENCE: B4883A  
; CURRENT APPLICATION NUMBER: US/10/139,794  
; CURRENT FILING DATE: 2002-05-06  
; PRIORITY NUMBER: US 60/288,885  
; PRIOR FILING DATE: 2001-05-04  
; NUMBER OF SEQ ID NOS: 2930  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: Translation of SEQ ID NO:9  
US-10-139-794-10  
Query Match Score 100.0%; DB 15; Length 146;  
Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 VPIQKVDITKLTKITVTRINDISHTQSSKQVTGDLTIPGHPILTSKMDQTAV 60  
Db 1 VPIQKVDITKLTKITVTRINDISHTQSSKQVTGDLTIPGHPILTSKMDQTAV 60  
Query 61 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPNASGLETLDSLGGVLBASGYS 120  
Db 61 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPNASGLETLDSLGGVLBASGYS 120  
Query 121 TEVVALSRQLQGSILWQDLSLSPGC 146  
Db 121 TEVVALSRQLQGSILWQDLSLSPGC 146

RESULT 3  
US-10-419-058-2  
; Sequence 2, Application US/10419058  
; Publication No. US20040053366A1  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Zhang, Jinyang  
; APPLICANT: Gillies, Stephen D.  
; TITLE OF INVENTION: Expression and Export of Anti-Obesity Proteins as PC  
; FILE REFERENCE: LEX-008  
; CURRENT FILING DATE: 2003-04-18  
; PRIORITY NUMBER: US/09/479,508  
; PRIOR APPLICATION NUMBER: US 60/115,079  
; PRIOR FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PRIOR FILING DATE: 0000-00-00

Query Match Score 100.0%; DB 15; Length 146;  
Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 VPIQKVDITKLTKITVTRINDISHTQSSKQVTGDLTIPGHPILTSKMDQTAV 60  
Db 1 VPIQKVDITKLTKITVTRINDISHTQSSKQVTGDLTIPGHPILTSKMDQTAV 60

RESULT 4  
US-10-467-114-1  
; Sequence 1, Application US/10467114  
; Publication No. US20040072219A1  
; GENERAL INFORMATION:  
; APPLICANT: Carr, Francis J.  
; APPLICANT: Carter, Graham  
; APPLICANT: Jones, Tim  
; APPLICANT: Williams, Stephen  
; APPLICANT: Hamilton, Anita  
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED IMMUNOGENICITY  
; FILE REFERENCE: MER-115  
; CURRENT APPLICATION NUMBER: US/10/467,114  
; CURRENT FILING DATE: 2003-08-05  
; PRIOR APPLICATION NUMBER: EP 01102618.4  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: EP 01103954.2  
; PRIOR FILING DATE: 2001-02-19  
; PRIOR APPLICATION NUMBER: PCT/EP02/01188  
; PRIOR FILING DATE: 2002-05-05  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-467-114-1  
Query Match Score 100.0%; DB 15; Length 146;  
Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 VPIQKVDITKLTKITVTRINDISHTQSSKQVTGDLTIPGHPILTSKMDQTAV 60  
Db 1 VPIQKVDITKLTKITVTRINDISHTQSSKQVTGDLTIPGHPILTSKMDQTAV 60

RESULT 5  
US-10-622-998-1  
; Sequence 1, Application US/10622998  
; Publication No. US20040105440A1  
; GENERAL INFORMATION:  
; APPLICANT: Kinstler, Olaf  
; APPLICANT: Ladd, David  
; APPLICANT: Papkov, Mikhail  
; TITLE OF INVENTION: PROTEIN CONJUGATES WITH A WATER-SOLUBLE BIOMATERIAL, BIODEGRADA  
; FILE REFERENCE: A-822  
; CURRENT APPLICATION NUMBER: US/10/622,998  
; CURRENT FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: 60/397,509  
; PRIOR FILING DATE: 2002-07-19  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1

LENGTH: 146  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-622-998-1

Query Match Score 736; DB 16; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKLTIKTTTRINDISHQSISQVSKQVTKGLDFPGLPLTLISKMDQTAV 60  
 Db 1 VPIQKVDDTKLTIKTTTRINDISHQSISQVSKQVTKGLDFPGLPLTLISKMDQTAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENLRDLHVLAFSKSCHLPWAGLETDSLGVLEASGYS 120  
 Db 61 YQQILTSMPSRNVIQISNDLENLRDLHVLAFSKSCHLPWAGLETDSLGVLEASGYS 120

Qy 121 TEVVALSRLOGSLQDMNQWLDLSPGC 146  
 Db 121 TEVVALSRLOGSLQDMNQWLDLSPGC 146

RESULT 6  
 US-10-658-814A-211  
 ; Sequence 211, Application US/10658834A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gantier, Rene  
 ; APPLICANT: Guyon, Thierry  
 ; APPLICANT: Drittanti, Lila  
 ; APPLICANT: Vega, Manuel  
 ; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu  
 ; TITLE OF INVENTION: Acid  
 ; TITLE OF INVENTION: Molecules and Related Applications  
 ; FILE REFERENCE: 38751-322  
 ; CURRENT APPLICATION NUMBER: US/10/658, 834A  
 ; CURRENT FILING DATE: 2003-09-08  
 ; PRIOR APPLICATION NUMBER: 60/1457, 135  
 ; PRIOR FILING DATE: 2003-03-21  
 ; PRIOR APPLICATION NUMBER: 60/1409, 898  
 ; PRIOR FILING DATE: 2002-09-09  
 ; NUMBER OF SEQ ID NOS: 1306  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 211  
 ; LENGTH: 146  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: Genbank AAA60470  
 ; DATABASE ENTRY DATE: 1995-01-13  
 ; US-10-658-814A-211

Query Match Score 736; DB 16; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKLTIKTTTRINDISHQSISQVSKQVTKGLDFPGLPLTLISKMDQTAV 60  
 Db 1 VPIQKVDDTKLTIKTTTRINDISHQSISQVSKQVTKGLDFPGLPLTLISKMDQTAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENLRDLHVLAFSKSCHLPWAGLETDSLGVLEASGYS 120  
 Db 61 YQQILTSMPSRNVIQISNDLENLRDLHVLAFSKSCHLPWAGLETDSLGVLEASGYS 120

Qy 121 TEVVALSRLOGSLQDMNQWLDLSPGC 146  
 Db 121 TEVVALSRLOGSLQDMNQWLDLSPGC 146

GENERAL INFORMATION:  
 ; APPLICANT: Carr, Francis J.  
 ; APPLICANT: Carter, Graham  
 ; APPLICANT: Jones, Tim  
 ; APPLICANT: Williams, Stephen  
 ; APPLICANT: Hamilton, Anita  
 ; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL EPITODES AND USE FOR PREPARING MOLECULES WITH REDUCED IMMUNOGENICITY  
 ; TITLE OF INVENTION: EPITODES AND USE FOR PREPARING MOLECULES WITH REDUCED  
 ; FILE REFERENCE: MER-117  
 ; CURRENT APPLICATION NUMBER: US/10/468, 496  
 ; CURRENT FILING DATE: 2003-09-25  
 ; PRIOR APPLICATION NUMBER: 0110354.2  
 ; PRIOR FILING DATE: 2001-02-19  
 ; PRIOR APPLICATION NUMBER: 0110577.5  
 ; PRIOR FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: 01106538.0  
 ; PRIOR FILING DATE: 2001-03-15  
 ; PRIOR APPLICATION NUMBER: 01106536.4  
 ; PRIOR FILING DATE: 2001-03-15  
 ; PRIOR APPLICATION NUMBER: 01107012.5  
 ; PRIOR FILING DATE: 2001-03-20  
 ; PRIOR APPLICATION NUMBER: 01106839.6  
 ; PRIOR FILING DATE: 2001-03-20  
 ; NUMBER OF SEQ ID NOS: 2036  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 1  
 ; LENGTH: 146  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; US-10-468-496-1

Query Match Score 736; DB 16; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKLTIKTTTRINDISHQSISQVSKQVTKGLDFPGLPLTLISKMDQTAV 60  
 Db 1 VPIQKVDDTKLTIKTTTRINDISHQSISQVSKQVTKGLDFPGLPLTLISKMDQTAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENLRDLHVLAFSKSCHLPWAGLETDSLGVLEASGYS 120  
 Db 61 YQQILTSMPSRNVIQISNDLENLRDLHVLAFSKSCHLPWAGLETDSLGVLEASGYS 120

Qy 121 TEVVALSRLOGSLQDMNQWLDLSPGC 146  
 Db 121 TEVVALSRLOGSLQDMNQWLDLSPGC 146

RESULT 8  
 US-10-872-198-127  
 ; Sequence 127, Application US/10872198  
 ; Publication No. US2005002897A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ulrich HAUPPS  
 ; APPLICANT: Andre KOLTERMANN  
 ; APPLICANT: Andreas SCHEIDIG  
 ; APPLICANT: Christian VOETMEIER  
 ; APPLICANT: Ulrich Kettling  
 ; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF  
 ; FILE REFERENCE: 04156.000U4  
 ; CURRENT APPLICATION NUMBER: US/10/872, 198  
 ; CURRENT FILING DATE: 2004-06-18  
 ; PRIOR APPLICATION NUMBER: 60/543, 518  
 ; PRIOR FILING DATE: 2004-02-11  
 ; PRIOR APPLICATION NUMBER: 60/524, 960  
 ; PRIOR FILING DATE: 2003-11-25  
 ; PRIOR APPLICATION NUMBER: EP 04003058  
 ; PRIOR FILING DATE: 2004-02-11  
 ; PRIOR APPLICATION NUMBER: EP 03035871  
 ; PRIOR FILING DATE: 2003-11-11  
 ; PRIOR APPLICATION NUMBER: EP 03025851  
 ; PRIOR FILING DATE: 2003-11-10

RESULT 7  
 US-10-468-496-1  
 ; Sequence 1, Application US/10468496  
 ; Publication No. US20040180386A1

PRIOR APPLICATION NUMBER: EP 03013819  
 PRIOR FILING DATE: 2003-06-18  
 NUMBER OF SEQ ID NOS: 149  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 127  
 LENGTH: 146  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-872-198-127

Query Match 100.0%; Score 736; DB 16; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKQDPTKLIKIVTRINDISHTQSVKVTKGDFPGLHPILTLSKMDQTAV 60  
 Db 1 VPIQKQDPTKLIKIVTRINDISHTQSVKVTKGDFPGLHPILTLSKMDQTAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPWASGLETDLSGGVLEASGYS 120  
 Db 61 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPWASGLETDLSGGVLEASGYS 120

Qy 121 TEVVALSRQLGSQSLQDMWQDLSPGC 146  
 Db 121 TEVVALSRQLGSQSLQDMWQDLSPGC 146

RESULT 9  
 US-10-623-119-1  
 Sequence 1, Application US/10/623189  
 Publication No. US200500204961  
 GENERAL INFORMATION  
 APPLICANT: DEPAOLI, Blif Arioqiu  
 APPLICANT: TAYLOR, Simeon I.  
 APPLICANT: OPAL, Blif Arioqiu  
 APPLICANT: GARG, Abhimanu  
 APPLICANT: TAYLOR, Simeon I.  
 TITLE OF INVENTION: USE OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETERMINING LIPOATROPHY  
 TITLE OF INVENTION: PREDISPOSITION TO SAID TREATMENT  
 FILE REFERENCE: 5A113 .8005 .US02  
 CURRENT APPLICATION NUMBER: US/10/623.189  
 CURRENT FILING DATE: 2003-07-18  
 PRIOR APPLICATION NUMBER: US 10/279,129  
 PRIOR FILING DATE: 2002-10-22  
 PRIOR APPLICATION NUMBER: US 60/336,394  
 PRIOR FILING DATE: 2001-10-22  
 NUMBER OF SEQ ID NOS: 2  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 1  
 LENGTH: 146  
 TYPE: PRT  
 FEATURE: Artificial Sequence  
 OTHER INFORMATION: Recombinant Leptin Human 146 (rhLe-Leptin 1-146)

US-10-623-189-1

Query Match 100.0%; Score 736; DB 17; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKQDPTKLIKIVTRINDISHTQSVKVTKGDFPGLHPILTLSKMDQTAV 60  
 Db 1 VPIQKQDPTKLIKIVTRINDISHTQSVKVTKGDFPGLHPILTLSKMDQTAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPWASGLETDLSGGVLEASGYS 120  
 Db 61 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPWASGLETDLSGGVLEASGYS 120

Qy 121 TEVVALSRQLGSQSLQDMWQDLSPGC 146  
 Db 121 TEVVALSRQLGSQSLQDMWQDLSPGC 146

RESULT 10

US-09-736-084-4  
 Sequence 4, Application US/09736084  
 Patent No. US00020107211A1  
 GENERAL INFORMATION  
 APPLICANT: THE ROCKEFELLER UNIVERSITY  
 TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC CORRESPONDENCE ADDRESS:  
 NUMBER OF SEQUENCES: 98  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/736,084  
 FILING DATE: 13-Dec-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/438,431  
 FILING DATE: May 10, 1995  
 APPLICATION NUMBER: 08/347,563  
 FILING DATE: NO. US20020107211A1ember 30, 1994  
 APPLICATION NUMBER: 08/282,345  
 FILING DATE: August 17, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-087 CIP21  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEFAX: 201 343-1684  
 TELEX: 133521  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 167 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: Human ob polypeptide  
 ORIGINAL SOURCE:  
 US-09-736-084-4

Query Match 100.0%; Score 736; DB 9; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-72;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKQDPTKLIKIVTRINDISHTQSVKVTKGDFPGLHPILTLSKMDQTAV 60  
 Db 22 VPIQKQDPTKLIKIVTRINDISHTQSVKVTKGDFPGLHPILTLSKMDQTAV 81

Qy 61 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPWASGLETDLSGGVLEASGYS 120  
 Db 82 YQQILTSMPSRNVIQISNDLENLRLHLVAFSKSCHLPWASGLETDLSGGVLEASGYS 141

Qy 121 TEVVALSRQLGSQSLQDMWQDLSPGC 146  
 Db 142 TEVVALSRQLGSQSLQDMWQDLSPGC 167

RESULT 11

US-09-928-522-7  
 Sequence 7, Application US/0928522  
 Patent No. US20020110857A1  
 GENERAL INFORMATION:  
 APPLICANT: Spurlock, Michael E.

TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID SEQUENCES CODING THEREFOR AND USES THEREOF

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: WHYTE HIRSCHBOECK DUDEK S.C.  
STREET: Suite 2100 111 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

ZIP: 53202

COMPUTER READABLE FORM:

  MEDIUM TYPE: Floppy disk

  COMPUTER: IBM PC compatible

  OPERATING SYSTEM: PC-DOS/MS-DOS

  SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

  APPLICATION NUMBER: US/09/928,522

  FILING DATE: 13-AUG-2001

  CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

  APPLICATION NUMBER: US/08/688,908

  FILING DATE: 31-JUL-1996

ATTORNEY/AGENT INFORMATION:

  NAME: Piotecher, Gary R.

REGISTRATION NUMBER: 27,830

REFERENCE/DOCKET NUMBER: PM-8808

TELECOMMUNICATION INFORMATION:

  TELEPHONE: 414-273-2100

  TELEFAX: 414-223-5000

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

  LENGTH: 167

  TYPE: amino acid

  STRANDEDNESS: <Unknown>

  TOPOLOGY: linear

  MOLECULE TYPE: protein

  SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-928-522-7

Query Match

  Score 736; DB 9; Length 167;

  Best Local Similarity 100.0%; Pred. No. 3.8e-72;

  Matches 146; Conservative 0; MisMatches 0; Gaps 0;

  Indels 0; Gaps 0;

  RESULT 13

  US-09-804-409A-11

  Sequence 11, Application US/09804409A

  Patent No. US2002015510A1

  GENERAL INFORMATION:

  APPLICANT: KIEFFER, TIMOTHY J.

  APPLICANT: CHEUNG, ANTHONY T.

  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN

  TITLE OF INVENTION: EXPRESSION IN GUTT

  FILE REFERENCE: 029996/027 8721

  CURRENT APPLICATION NUMBER: US/09/804,409A

  CURRENT FILING DATE: 2001-03-12

  NUMBER OF SEQ ID NOS: 18

  SOFTWARE: PatentIn Ver. 2.1

  SEQ ID NO 11

  LENGTH: 167

  TYPE: PRT

  ORGANISM: Homo sapiens

  US-09-804-409A-11

Query Match

  Score 736; DB 9; Length 167;

  Best Local Similarity 100.0%; Pred. No. 3.8e-72;

  Matches 146; Conservative 0; MisMatches 0; Gaps 0;

  Indels 0; Gaps 0;

  RESULT 14

  US-09-804-409A-11

  Sequence 11, Application US/09804409A

  Patent No. US2002015510A1

  GENERAL INFORMATION:

  APPLICANT: Hernday, Natasha

  TITLE OF INVENTION: Canine OB Protein Compositions and Methods

  NUMBER OF SEQUENCES: 5

  CORRESPONDENCE ADDRESS: Application US/0989306

  Patent No. US20102142456A1

  GENERAL INFORMATION:

  APPLICANT: Amgen Inc.

  STREET: One Amgen Center Drive

  CITY: Thousand Oaks

  STATE: California

  COUNTRY: U.S.A.

  ZIP: 91320

  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

  APPLICATION NUMBER: US/09/789,306

  FILING DATE: 20-Feb-2001

  CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

  APPLICATION NUMBER: 08/609,408

  FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

  NAME: Egerer, Joan D.

  REFERENCE/DOCKET NUMBER: A-387

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

  LENGTH: 167 amino acids

  TYPE: amino acid

  STRANDEDNESS: single

  TOPOLOGY: linear

  MOLECULE TYPE: protein

  SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-789-306-3

Query Match

  Score 736; DB 9; Length 167;

  Best Local Similarity 100.0%; Pred. No. 3.8e-72;

  Matches 146; Conservative 0; MisMatches 0; Gaps 0;

  Indels 0; Gaps 0;

  RESULT 15

  US-09-804-409A-11

  Sequence 11, Application US/09804409A

  Patent No. US2002015510A1

  GENERAL INFORMATION:

  APPLICANT: KIEFFER, TIMOTHY J.

  APPLICANT: CHEUNG, ANTHONY T.

  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN

  TITLE OF INVENTION: EXPRESSION IN GUTT

  FILE REFERENCE: 029996/027 8721

  CURRENT APPLICATION NUMBER: US/09/804,409A

  CURRENT FILING DATE: 2001-03-12

  NUMBER OF SEQ ID NOS: 18

  SOFTWARE: PatentIn Ver. 2.1

  SEQ ID NO 12

  LENGTH: 167

  TYPE: PRT

  ORGANISM: Homo sapiens

  US-09-804-409A-11

Query Match

  Score 736; DB 9; Length 167;

  Best Local Similarity 100.0%; Pred. No. 3.8e-72;

  Matches 146; Conservative 0; MisMatches 0; Gaps 0;

  Indels 0; Gaps 0;

  RESULT 16

  US-09-804-409A-11

  Sequence 11, Application US/09804409A

  Patent No. US2002015510A1

  GENERAL INFORMATION:

  APPLICANT: KIEFFER, TIMOTHY J.

  APPLICANT: CHEUNG, ANTHONY T.

  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN

  TITLE OF INVENTION: EXPRESSION IN GUTT

  FILE REFERENCE: 029996/027 8721

  CURRENT APPLICATION NUMBER: US/09/804,409A

  CURRENT FILING DATE: 2001-03-12

  NUMBER OF SEQ ID NOS: 18

  SOFTWARE: PatentIn Ver. 2.1

  SEQ ID NO 13

  LENGTH: 167

  TYPE: PRT

  ORGANISM: Homo sapiens

  US-09-804-409A-11

Query Match

  Score 736; DB 9; Length 167;

  Best Local Similarity 100.0%; Pred. No. 3.8e-72;

  Matches 146; Conservative 0; MisMatches 0; Gaps 0;

  Indels 0; Gaps 0;

  RESULT 17

  US-09-804-409A-11

  Sequence 11, Application US/09804409A

  Patent No. US2002015510A1

  GENERAL INFORMATION:

  APPLICANT: Hernday, Natasha

  TITLE OF INVENTION: Canine OB Protein Compositions and Methods

  NUMBER OF SEQUENCES: 5

  CORRESPONDENCE ADDRESS: Application US/0989306

  Patent No. US20102142456A1

  GENERAL INFORMATION:

  APPLICANT: Hernday, Natasha

  TITLE OF INVENTION: Canine OB Protein Compositions and Methods

  NUMBER OF SEQUENCES: 5

  CORRESPONDENCE ADDRESS: Application US/0989306

  Patent No. US20102142456A1

  GENERAL INFORMATION:

  APPLICANT: Amgen Inc.

  STREET: One Amgen Center Drive

  CITY: Thousand Oaks

  STATE: California

  COUNTRY: U.S.A.

  ZIP: 91320

  COMPUTER READABLE FORM:

RESULT 14

Db 82 YQQILTSMPSRNVIQISNDLNLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 141

Qy 121 TEVVALSRQLQSLQDMLWQDMLSPGC 146

Db 142 TEVVALSRQLQSLQDMLWQDMLSPGC 167

US-09-316-393-4

Sequence 4, Application US/09316393

Publication No. US20030040039A1

GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY

TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/316,393

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/292,345

FILING DATE: August 17, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson ESG, David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 497-5800

TELEFAX: 201 343-1684

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 167 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: Human Ob protein

ORIGINAL SOURCE: Human

US-09-316-393-4

Sequence 67, Application US/10440464

Publication No. US20040018528A1

GENERAL INFORMATION:

APPLICANT: DEPRIMO, SAMUEL

APPLICANT: O'FARRELL, ANNE-MARIE

APPLICANT: MORMOTO, ALYSSA

APPLICANT: SMOJICH, BEVERLY

APPLICANT: MANNING, WILLIAM

APPLICANT: WALTER, SARAH

APPLICANT: CHERINGTON, JULIE

APPLICANT: SCHILLING, JIM

TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE

CURRENT APPLICATION NUMBER: US/10/440,464

CURRENT FILING DATE: 2003-05-19

PRIOR APPLICATION NUMBER: 60/380,872

PRIOR FILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: 60/448,922

PRIOR FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: 60/448,874

PRIOR FILING DATE: 2003-02-24

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 67

LENGTH: 167

TYPE: PRT

ORGANISM: Homo sapiens

US-10-440-464-67

Query Match Score 736; DB 15; Length 167;

Best Local Similarity 100.0%; Pred. No. 3.8e-72; Mismatches 0; Indels 0; Gaps 0;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKITIVTRINDISHTQSVSQKVTGLDFIPGHPILTLSKMDQTLAV 60

Db 22 VPIQKVQDDTKTLIKITIVTRINDISHTQSVSQKVTGLDFIPGHPILTLSKMDQTLAV 81

Qy 61 YQQILTSMPSRNVIQISNDLNLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

Db 82 YQQILTSMPSRNVIQISNDLNLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 141

Qy 121 TEVVALSRQLQSLQDMLWQDMLSPGC 146

Db 142 TEVVALSRQLQSLQDMLWQDMLSPGC 167

Query Match Score 736; DB 10; Length 167;

Best Local Similarity 100.0%; Pred. No. 3.8e-72; Mismatches 0; Indels 0; Gaps 0;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKITIVTRINDISHTQSVSQKVTGLDFIPGHPILTLSKMDQTLAV 60

Db 22 VPIQKVQDDTKTLIKITIVTRINDISHTQSVSQKVTGLDFIPGHPILTLSKMDQTLAV 81

Qy 61 YQQILTSMPSRNVIQISNDLNLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

Db 82 YQQILTSMPSRNVIQISNDLNLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 141

Qy 121 TEVVALSRQLQSLQDMLWQDMLSPGC 146

Db 142 TEVVALSRQLQSLQDMLWQDMLSPGC 167

RESULT 15

US-10-440-464-67

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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:53:02 ; Search time 22.8562 Seconds  
(without alignments)

614.609 Million cell updates/sec

Title: US-10-049-182-6

Perfect score: 736

Sequence: 1 VPIQKVQDDTKTLIKTIVR.....SRIQGSIQDMLWQDLSPGC 146

Scoring table: Blosum62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database : PIR\_79:\*

1: pir1;\*

2: pir2;\*

3: pir3;\*

4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	167	1 LTHU	leptin precursor -
2	702.5	97.9	166	1 L53166	leptin precursor -
3	61.9	84.1	167	1 LTMS	leptin precursor -
4	60.5	82.2	167	1 LTRT	rat ob - rat
5	60.5	82.2	167	1 I55622	glutamate dehydrogen
6	81.5	11.1	1600	2 AB3281	hypothetical prote
7	80.5	10.9	444	2 S54039	probable myosin heavy
8	79	10.7	829	2 T01362	hypothetical prote
9	79	10.7	952	2 H84583	sensory transducti
10	78	10.6	420	2 S75514	probable soluble
11	78	10.6	639	2 AI0055	phosphotransferase
12	77.5	10.5	574	1 B42374	ribosomal protein
13	76.5	10.4	173	2 S77486	carbamoyl-phosphatase
14	76.5	10.4	362	2 A83967	probable trehalose
15	76.5	10.4	822	2 E86305	hypothetical prote
16	76	10.3	409	2 B89954	5,10-methylentetra
17	76	10.3	570	2 T46011	glutamate-1-semial
18	76	10.3	1036	2 D70117	beta transducin-like
19	75.5	10.3	403	2 T26551	hypothetical prote
20	75.5	10.3	1438	2 S59792	probable membrane
21	75	10.2	142	2 C72430	hypothetical prote
22	75	10.2	296	2 D70424	5,10-dihydroxy-1,4-d
23	75	10.2	424	2 E81359	prolactin, 20 kDa
24	75	10.2	1191	2 S7644	prolactin II precur
25	74.5	10.1	559	2 AB2202	expolysaccharide
26	74.5	10.1	674	2 S46092	alkaline phosphatase
27	74	10.1	177	2 A28106	hypothetical prote
28	74	10.1	200	2 B32477	probable membrane
29	74	10.1	421	2 AB2959	hypothetical prote

## ALIGNMENTS

RESULT 1

LTHU leptin precursor - human

N: Alternative names: obese protein; obesity factor

C: Species: Homo sapiens (man)

C: Accession: A38922; JE0148

R: Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Friedman, J.M. Nature 372, 425-432, 1994

A: Title: Positional cloning of the mouse obese gene and its human homologue.

A: Reference number: SS0863; PMID:95075453; PMID:7984236

A: Accession: A38922

A: Status: preliminary; nucleic acid sequence not shown

A: Molecule type: mRNA

A: Residues: 1-167 <ZHA>

A: Cross-references: UNIPROT:P41159; GB:U16915; NID:9623331; PIDN:AAA60470.1; PID:962333

R: Liao, H.J.; Deng, Y.B.; Chen, X.M.; Ye, Y.Z. Chinese Biochem. J. 13, 249-253, 1997

A: Title: Cloning of chinese obesity gene and construction of prokaryotic expression vec

A: Reference number: JE0148

A: Accession: JE0148

A: Molecule type: mRNA

A: Residues: 'M' 22-167 <LIA>

A: Experimental source: adipose tissue

A: Note: the author translated GAC for residue 148 as Ser

C: Genetics:

A: Gene: GDB:LEP; OB; OBS

A: Cross-references: GDB:136420; OMIM:164160

A: Map position: 7q31.3-7q31.3

C: Superfamily: leptin

C: Keywords: adipose tissue

F: 21/Domain: signal sequence #status predicted <MAI>

F: 22/16/Domain: signal sequence #status predicted <SIG>

F: 22/16/Domain: leptin #status predicted <MAI>

RESULT 2

153166 Leptin precursor - human  
 N:Alternate names: obese protein  
 C:Species: Homo sapiens (man)  
 C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
 C:Accession: I53166; GO2328  
 R:Masuzaki, H.; Ogawa, Y.; Isse, N.; Satoch, N.; Okazaki, T.; Shigemoto, M.; Mori, K.; Ta  
 Diabetes 44, 855-858, 1995  
 A;Title: Human obese gene expression. Adipocyte-specific expression and regional differenc  
 A;Reference number: I53166; MUID:95309556; PMID:7799654  
 A;Accession: I53166  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-166 <REB>  
 A;Cross-references: UNIPROT:P41159; GB:D49487; PIDN:BAA08448.1; PID:9904212  
 R;Chehab, F. F.; Lim, M. E.  
 submitted to the EMBL Data Library, December 1995  
 A;Reference number: HO1063  
 A;Accession: GO2328  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-166 <CHB>  
 A;Cross-references: EMBL:U43415; NID:91163105; PIDN: AAC31660.1; PID:91163106  
 C;Genetics:  
 A;Gene: GDB:LEP; OB; OBS  
 A;Cross-references: GDB:136420; OMIM:164160  
 A;Map position: 7q32.1-7q32.1  
 A;Introns: 4/8  
 C;Superfamily: leptin  
 Query Match Score 720.5; DB 2; Length 166;  
 Best Local Similarity 99.3%; Pred. No. 4.6e-59;  
 Matches 145; Conservative 0; Indels 1; Gaps 1;  
 C;Superfamily: leptin  
 Qy 1 VPIQKVQDDTKEIYTRINDISHTQSVSQKQVTKGDFPGLHPILTISKMDTLLAV 60  
 Db 22 VPIQKVQDDTKEIYTRINDISHT-SVSSQKQVTKGDFPGLHPILTISKMDTLLAV 80  
 Qy 61 YQQILTSMPSRNVIQISNDLENLRDILHVLASFSKSLPQWASGLETDLSGGVLEASGYS 120  
 Db 81 YQQILTSMPSRNVIQISNDLENLRDILHVLASFSKSLPQWASGLETDLSGGVLEASGYS 140  
 Qy 121 TEVVALSRQLQSLQDMILWQDLSPGC 146  
 Db 141 TEVVALSRQLQSLQDMILWQDLSPGC 166

RESULT 4  
 Leptin precursor - rat  
 N:Alternate names: obese protein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 21-Jul-1995 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
 C:Accession: PC4034; JC4142  
 R;Funahashi, T.; Shimomura, I.; Hiraoka, H.; Arai, T.; Takahashi, M.; Nakamura, T.; Noz  
 Biochem. Biophys. Res. Commun. 211, 469-475, 1995  
 A;Title: Enhanced expression of rat obese (ob) gene in adipose tissues of ventromedial  
 A;Reference number: PC4034; MUID:95314614; PMID:7794258  
 A;Accession: PC4034  
 A;Molecule type: mRNA  
 A;Residues: 1-167 <FUN>  
 A;Cross-references: UNIPROT:P50596  
 A;Experimental source: adipose tissue  
 R;Murakami, T.; Shima, K.  
 A;Note: The authors translated the codon AAA for residue 32 as Thr  
 Biochem. Biophys. Res. Commun. 209, 944-952, 1995  
 A;Title: Cloning of rat obese cDNA and its expression in obese rats  
 A;Reference number: JC4142; MUID:95315175; PMID:7733988  
 A;Accession: JC4142  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-167 <MR>  
 A;Cross-references: DDBJ:D49653; NID:9995614; PIDN:BAA08529.1; PID:9995615  
 A;Experimental source: liver  
 C;Comment: This protein is proposed to function as part of a signalling pathway from ad:  
 A;Genes: obese  
 C;Keywords: adipose tissue  
 F;1-21/Domain: signal sequence #status predicted <SIG>  
 F;22-167/Product: leptin #status predicted <MAT>

Query Match Score 82.2%; Score 605; DB 1; Length 167;  
 Best Local Similarity 83.6%; Pred. No. 1.3e-47;  
 Matches 122; Conservative 13; Mismatches 11; Indels 0; Gaps 0 ;

Qy 1 VPIQKVQDDTKEIYTRINDISHTQSVSQKQVTKGDFPGLHPILTISKMDTLLAV 60  
 Db 22 VPIQKVQDDTKEIYTRINDISHT-SVSSQKQVTKGDFPGLHPILTISKMDTLLAV 80  
 Qy 61 YQQILTSMPSRNVIQISNDLENLRDILHVLASFSKSLPQWASGLETDLSGGVLEASGYS 120  
 Db 82 YQQILTSMPSRNVIQISNDLENLRDILHVLASFSKSLPQWASGLETDLSGGVLEASGYS 140  
 Qy 121 TEVVALSRQLQSLQDMILWQDLSPGC 146  
 Db 142 TEVVALSRQLQSLQDMILWQDLSPGC 167

RESULT 5  
 Leptin precursor - mouse  
 N:Alternate names: obese protein  
 C:Species: Mus musculus (house mouse)  
 C:Accession: S50863  
 R;Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.  
 Nature 372, 425-432, 1994  
 A;Title: Positional cloning of the mouse obese gene and its human homologues.  
 A;Reference number: S50863; MUID:95075453; PMID:7984236  
 A;Accession: S50863  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-167 <ZIR>  
 A;Cross-references: UNIPROT:P41160; EMBL:U18812; PIDN:AAA64564.1; PID:96032  
 C;Keywords: adipose tissue  
 F;1-21/Domain: signal sequence #status predicted <SIG>  
 F;22-167/Product: leptin #status predicted <MAT>

Query Match Score 84.1%; Score 619; DB 1; Length 167;  
 Best Local Similarity 84.9%; Pred. No. 7.1e-49;  
 Matches 124; Conservative 13; Mismatches 9; Indels 0; Gaps 0 ;

Qy 1 VPIQKVQDDTKEIYTRINDISHTQSVSQKQVTKGDFPGLHPILTISKMDTLLAV 60



euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
 A;Reference number: A84420; PMID:20083487; PMID:10617197  
 A;Accession: CB4760  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-829 <STO>  
 A;Cross-references: GB:AE002093; NID:93132472; PIDN: AAC16261.1; GSPDB:GN00139  
 A;Gene: At2g34730; T29F13.6  
 A;Map position: 2  
 A;Introns: 728/2; 770/3

Query Match 10.7%; Score 79; DB 2; Length 829;  
 Best Local Similarity 21.5%; Pred. No. 40;  
 Matches 34; Conservative 27; Mismatches 45; Indels 52; Gaps 6;  
 Db 57 ISRVSVD-SIIRGMVTAES-----DAABEIAQKD-----DELSKIRETLLYH 99  
 Qy 62 -----QQLTSMPSRNVIQISNDLENLRLDHVLAFSKSCHL 99  
 Db 100 VGSSEENNESSESRLIHDELTOGSSSSSLRKARQMLMVEELTNLREYTHIN----- 150  
 Qy 100 WSGGLETDLSLGVLLEASGYSTEVVALSRQLQSDML 137  
 Db 151 -GSGATVDSLGL--LDSSPHETRSRTVDKMQLDSLKSTL 185

## RESULT 9

H84583 hypothetical protein At2g20010 [Imported] - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C;Accession: HB84583  
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Umayam, L.; Fallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
 A;Reference number: A84420; PMID:20083487; PMID:10617197  
 A;Accession: HB84583  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-952 <STO>  
 A;Cross-references: UNIPROT:Q9SL80; GB:AE002093; NID:94580471; PIDN: AAC24395.1; GSPDB:GN  
 C;Genetics:  
 A;Gene: At2g20010  
 A;Map position: 2

Query Match 10.7%; Score 79; DB 2; Length 952;  
 Best Local Similarity 33.3%; Pred. No. 48;  
 Matches 23; Conservative 15; Mismatches 19; Indels 12; Gaps 3;  
 Db 45 LHPILTSKMPDTLAVYQQQLTSMPSR-NVIQISNDLENLRLDHVLAFL-----SK 94  
 Db 186 LYPCVPNLSKDSRVQQLQITRSGLERPLDGTKITGTNLRSLVMSLASRQNNGIGSE 245  
 Qy 95 SCHLPWASG 103  
 Db 246 TCH-WADL 252

Query Match 10.6%; Score 78; DB 2; Length 420;  
 Best Local Similarity 28.2%; Pred. No. 21;  
 Matches 33; Conservative 18; Mismatches 44; Indels 22; Gaps 5;  
 Db 29 PRLHILL-----LEDNLAAERLLQEILKGSPKPNF-AFNHQVRLGDALTVLAQGEKEFDII 82

Qy 95 --SCHLPWASGLTWDLSLGG----VLEASGYSTEVVALSRQLQSGSFLQDMILWQDLS 143  
 Db 83 LLDDLTEDSQGLNSLPQLQSHFPQNLPPIIVLTHYQDSEBELAVERQGAQDYLWKRDVD 139

## RESULT 11

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O., K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*:  
 A;Reference number: S74322; PMID:97061201; PMID:8905231  
 A;Accession: S75514  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-420 <KAN>  
 A;Cross-references: UNIPROT:P74004; EMBL:D90911; NID:91652083; PIDN:BAA180;  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C;Genetics:  
 A;Start codon: GTG  
 C;Superfamily: sensory transduction system regulatory protein; response regulator homolog  
 C;Keywords: phosphoprotein  
 F;33-146/Domain: response regulator homology <RRH>  
 F;85/Binding site: Phosphate (Asp) (covalent) #status predicted

Query Match 10.6%; Score 78; DB 2; Length 420;  
 Best Local Similarity 28.2%; Pred. No. 21;  
 Matches 33; Conservative 18; Mismatches 44; Indels 22; Gaps 5;  
 Db 29 PRLHILL-----LEDNLAAERLLQEILKGSPKPNF-AFNHQVRLGDALTVLAQGEKEFDII 82

Qy 43 PCLHPILTSKMPDTLAVYQQQLTSMPSR-NVIQISNDLENLRLDHVLAFLFSK----- 94  
 Db 29 PRLHILL-----LEDNLAAERLLQEILKGSPKPNF-AFNHQVRLGDALTVLAQGEKEFDII 82

Qy 95 --SCHLPWASGLTWDLSLGG----VLEASGYSTEVVALSRQLQSGSFLQDMILWQDLS 143  
 Db 83 LLDDLTEDSQGLNSLPQLQSHFPQNLPPIIVLTHYQDSEBELAVERQGAQDYLWKRDVD 139

RESULT 12

A;0055 probable soluble lytic murein transglycosylase (EC 3.2.1.-) [imported] - *Yersinia pestis*  
 C;Species: *Yersinia pestis*  
 C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C;Accession: A10055  
 R;Parthill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature 413, 523-527, 2001  
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A;Reference number: AB00001; Yersinia pestis, the causative agent of plague.  
 A;Accession: A10055  
 A;Gene: YPO0452  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-639 <KUR>  
 A;Cross-references: UNIPROT:Q8ZIP2; GB:AL590842; PIDN:GAC89308.1; GSPDB:GN  
 C;Genetics:  
 A;Start codon: ATG  
 C;Superfamily: soluble lytic transglycosylase  
 C;Keywords: glycosidase; hydrolase

Query Match 10.6%; Score 78; DB 2; Length 639;  
 Best Local Similarity 23.0%; Pred. No. 35;  
 Matches 32; Conservative 21; Mismatches 38; Indels 48; Gaps 5;  
 Db 69 TQDLSDVSTAGVKDFL-NRHPTLPPRK-----SLPSRFV---NELARREDW 110

Qy 27 TQSVSSKQKVTLGDFIPGLHPILTLISKMDQTLLAVYQQILTSMPSPRNVIQISNDLENLRLDH 86  
 Db 87 LHVLAFSKSCLP-----WASGLETL-----DSIGGYLEA 116

Qy 111 RGLLTSPTAKPVAACTNYYYAKVATGEOSVAVRGASEIWLNCGQLPGSCKLSSVWQO 170

S75514 sensory transduction histidine kinase srl1324 - *Synechocystis* sp. (strain PCC 6803)  
 C;Alternate names: protein srl1324  
 A;Variety: PCC 6803  
 C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
 C;Accession: S75514

RESULT 12  
 B42374

phosphotransferase system enzyme I (EC 2.7.3.9) - *Staphylococcus carnosus*  
 C;Species: *Staphylococcus carnosus*  
 C;Date: 10-Jul-1992 #sequence\_revision 31-Jan-1997 #text\_change 09-Jul-2004  
 C;Accession: B42374; S17075  
 R;J: Bacteriol. 174, 2208-2214, 1992  
 A;Title: *Staphylococcal phosphoenolpyruvate-dependent phosphotransferase system: molecular studies of the gene product.*  
 A;Reference number: A42374; MUID:92202148; PMID:1551842  
 A;Accession: B42374  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-54 <EIS>  
 A;Cross-references: UNIPROT:P21533; GB:M69050; PIDN:CAA4117\_1; PID:946909  
 C;Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I homology <PTI>  
 C;Keywords: phosphoprotein; phosphotransferase; sugar transport system  
 P;P-563/Domain: phosphotransferase system enzyme I homology <PTI>  
 A;Accession: S15367; MUID:91200066; PMID:1901791  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-90  
 A;Cross-references:  
 C;Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I homology <PTI>  
 C;Keywords: phosphotransferase; sugar transport system  
 P;P-563/Domain: phosphotransferase system enzyme I homology <PTI>  
 Query Match 10.5%; Score 77.5; DB 1; Length 574;  
 Best Local Similarity 25.0%; Pred. No. 34;  
 Matches 32; Conservative 27; Mismatches 54; Indels 15; Gaps 5;  
 Qy 11 KTLIKTVTR--INDISHTQSSVSSKOKVTGFLDPIPOLHPILTSKMDQTLLAVYQQILTS 67  
 Db 188 RTSHSALMRSRLSLEPAVVGRTSITEEVAGDTIVVDMTGDVLINPSDEVIAEYQEE--- 243  
 Qy 68 MFSRNTVQISNDLNRDHLVAFSKSCHLPWASGLETLDLSGGVLE--ASG---YSTE 122  
 Db 244 -KRENFFPKDKQELQRDAESVTA-DGHAVELAANIGTPNDLPGVIENGAEIGLHYRTE 300  
 Qy 123 VVALSRLQ 130  
 Db 301 FLYMGRDQ 308  
 RESULT 13  
 S77486 ribosomal protein S5 - *Synechocystis* sp. (strain PCC 6803)  
 N;Alternate names: protein sll1812  
 C;Species: *Synechocystis* sp.  
 C;Variety: PCC 6803  
 C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
 C;Accession: S77486  
 C;Keywords: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-173 <PTN>  
 A;Cross-references: UNIPROT:P73304; EMBL:D90905; GB:AB001339; NID:91652360; PIDN:BAA173  
 A;Gene: rpS5  
 C;Superfamily: ribosomal protein S5/S2  
 C;Keywords: protein biosynthesis; ribosome  
 Query Match 10.4%; Score 76.5; DB 2; Length 173;  
 Best Local Similarity 20.2%; Pred. No. 9; Gaps 3;  
 Matches 29; Conservative 12; Mismatches 41; Indels 11; Gaps 3;

Mon Mar 14 08:10:18 2005

us-10-049-182-6.rpr

Page 6

Db 470 GLDEMSENGIPESEMOM----RKITPLQLPQQDVTCQYSQSNN----RLITLGFFCTLA 521  
Qy 98 LPWASGLFLD----SLGGVLEA--SGYSTEVVAISR 128  
Db 522 EPNSGTREMDLKINPELKGTALKALCNBPKTRVVVLSR 559

Search completed: March 12, 2005, 05:04:36  
Job time : 23.8562 secs

Scoring table:	BLOSUM62	ALIGMENTS		
Gapopen:	10.0			
Sequences:	1 VPIQKVQDDTKTLIKTIVTR.....SRUQGSILQDMLWQDLSPGC 146			
Scoring table:	BLOSUM62			
Gapopen:	10.0			
Sequences:	1612378 seqs, 512079187 residues			
Total number of hits satisfying chosen parameters:	1612378			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0% Maximum Match 100%			
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES	*			
Result No.	Score	Query		
Length	Match	DB ID		
Description				
1	736	100.0	167 1 OB_HUMAN	P41159 homo sapien
2	736	100.0	167 2 OB_PANTR	O67158 homo sapien
3	733	99.6	146 1 OB_GORGO	O07750 pan troglod
4	728	98.9	146 1 OB_PONY	Q92189 gorilla gor
5	721	98.0	146 1 OB_MACMU	Q92334 pongo pygma
6	672	91.3	167 1 OB_FELCA	Q25054 macaca mulia
7	679	86.8	146 2 Q678r8	Q92121 felis silv
8	628	85.3	167 1 OB_BOVIN	O678r8 bubalus bub
9	628	85.3	167 1 OB_PIG	P55095 bos taurus
10	627	85.2	167 1 OB_SHEEP	Q24066 sus scrofa
11	624	84.8	146 1 OB_MOUSE	O26603 ovis aries
12	619	84.1	167 1 OB_RAT	P41160 mus musculus
13	605	82.2	167 1 OB_CANFA	Q50596 rattus norvegicus
14	598	81.0	167 1 OB_CHICK	O07220 canis familiaris
15	586.5	79.7	163 1 OB_MELGA	O41164 gallus gallus
16	576.5	78.3	145 1 OB_EQUUS	Q94116 meles meles
17	522.5	71.0	145 2 Q678r2	Q678r2 equus caballus
18	505	68.6	167 1 OB_SMICR	Q95sw9 smithopsis
19	498	67.7	119 2 Q861R2	Q861R2 bubalus bubalis
20	477	64.8	118 2 Q8Mf60	OBMf60 alopech laevis
21	476	64.7	118 2 Q8Mf58	Q8Mf58 vulpes vulpes
22	474	64.4	118 2 Q8Mf59	Q8Mf59 nyctereutes
23	463	63.7	118 2 Q8Mf61	Q8Mf61 canis familiaris
24	465	63.2	167 2 Q706D0	Q706D0 halichoerus
25	463	62.9	167 2 Q706D1	Q706D1 phoca vitulina
26	462	62.8	123 2 Q95Kw9	Q95Kw9 myotis lucifugus
27	449	61.0	109 2 Q866S7	Q866S7 bubalus bubalis
28	447	60.7	99 1 OB_HORSE	Q9t009 equus caballus
29	439	59.6	109 2 Q864V1	Q864V1 camelus dromedarius
30	387	52.6	106 2 Q95Nc5	Q95Nc5 capra hircus
31	380	51.6	90 2 Q8Wmk7	Q8Wmk7 delphinapterus



Qy	1 VPIQKQDDTTRKLTKTIVTRNVIQISNDLENLRLHLYFLPSKSCSCLPWAISGLTLDLSGCVLPIHTLSKMDOTLAV 60
Db	61 YQQILTSMSPRSNVIQISNDLENLRLHLYFLPSKSCSCLPWAISGLTLDLSGCVLPIHTLSKMDOTLAV 60
Qy	61 YQQILTSMSPRSNVIQISNDLENLRLHLYFLPSKSCSCLPWAISGLTLDLSGCVLPIHTLSKMDOTLAV 60
Db	121 TEVVALSRQLQGSQDMLWQDLSPGC 146
Qy	121 TEVVALSRQLQGSQDMLWQDLSPGC 146
Db	121 TEVVALSRQLQGSQDMLWQDLSPGC 146
<b>RESULT 4</b>	
DB_GORG	GORG
ID	OB_091189;
AC	091189;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Leptin (Obesity factor).
OS	Synonyms-OB;
OC	Name=LEP; Gorilla gorilla (Lowland Gorilla).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX	NCBI_TaxID=995;
RN	SEQUENCE FROM N.A.
RRP	Smith D.P., Zhang X., Hsiung H.M., Submitted (Oct-1996) to the EMBL/GenBank/DDJB databases.
RRL	- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By similarity).
CC	-1- SUBCELLULAR LOCATION: Secreted (Probable).
CC	-1- SIMILARITY: Belongs to the leptin family.
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DR	EMBL; U72872; AAB17091.1; -.
DR	HSSP; P41159; JAX8.
DR	InterPro; IPR009079; 4_helix_cytokine.
DR	InterPro; IPR000065; Leprin.
DR	Pfam; PF02024; Leptin; 1.
DR	PRINTS; PR00495; LEPTIN.
DR	ProDom; PD005698; Leptin; 1.
KW	Obesity.
DISM.FID	96 146 BY similarity
SEQUENCE	146 AA; 16031 MW; 02C43BF69A4C89C CRC64;
SQ	Query Match 98.3%; Score 728; DB 1; Length 146;
Best Local Similarity 98.6%; Pred. No. 5e-59; Mismatches 0; Indels 0; Gaps 0	
Qy	1 VPIQKQDDTTRKLTKTIVTRNVIQISNDLENLRLHLYFLPSKSCSCLPWAISGLTLDLSGCVLPIHTLSKMDOTLAV 60
Db	1 VPIQKQDDTTRKLTKTIVTRNVIQISNDLENLRLHLYFLPSKSCSCLPWAISGLTLDLSGCVLPIHTLSKMDOTLAV 60
Qy	61 YQQILTSMSPRSNVIQISNDLENLRLHLYFLPSKSCSCLPWAISGLTLDLSGCVLPIHTLSKMDOTLAV 60
Db	61 YQQILTSMSPRSNVIQISNDLENLRLHLYFLPSKSCSCLPWAISGLTLDLSGCVLPIHTLSKMDOTLAV 60
Qy	121 TEVVALSRQLQGSQDMLWQDLSPGC 146
Db	121 TEVVALSRQLQGSQDMLWQDLSPGC 146

RESULT 5					
OB_PONY		STANDARD		PRT;	
ID	OB_PONY				146 AA.
AC	Q95334;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DB	Lepin (Obesity factor).				
GN	Name=LEP; Synonyms=OB;				
OS	Pongo pygmaeus (Orangutan).				
OC	Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;				
OC	Primates; Catarrhini; Hominoidea; Pongo.				
OX	NCBI_TAXID=9600;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Schöner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,				
RA	Rockey P.K., Rosteck P.R.;				
RT	"Cloning of obese genes from different species: a comparison of the gene structures and the sequences of the obese gene products, Lepin."				
RT	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.				
RT	- - FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By similarity).				
CC	- - SUBCELLULAR LOCATION: Secreted (Probable).				
CC	- - SIMILARITY: Belongs to the Leptin family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> or send an email to license@isb-sib.ch).				
CC	EMBL; U72873; AAB17092; 1; -.				
DR	HSSP; P41159; TAX8.				
DR	InterPro; IPR009079; 4 helix cytokine.				
DR	InterPro; IPR000065; Leptin.				
DR	Pfam; PF02024; Leptin_1.				
PRINTS	PR00455; LBPTIN.				
DR	ProDom; PD005698; Leptin_1.				
KW	Obeesity.				
FT	DISULFID. 96 146 MW. By similarity.				
SQ	SEQUENCE 146 AA; 16195 MW; 3F50A1338PFBD4 CRC64;				
Query	Match 98.0%; Score 721; DB 1; Length 146;				
Best Local Similarity 97.3%; Pred. No. 2 2e-58;					
Matches 142; Conservative 2; Mismatches 2; Indels 0; Gaps 0					
Qy 1 VPIQKQDDDTKLTKITVTRINDIHTQSUSKQKVTVGLDFIPGHLPIITLSKMDTLLAV 60					
Db 1 VPIQKQDDDTKLTKITVTRINDIHTQSUSKQKVTVGLDFIPGHLPIITLSKMDTLLAV 60					
Qy 61 YQQILTSMPSRNVIQISNDLENRLILHVAFLPSKCHLPASGLETLDSLGGVLBASGYS 120					
Db 61 YQQILTSMPSRNVIQISNDLENRLILHVAFLPSKCHLPASGLETLDSLGGVLBASGYS 120					
Qy 121 TEVVVALSRLOGSLQDMWLQDLSPGC 146					
Db 121 TEVVVALSRLOGSLQDMWLQDLSPGC 146					



Leptin precursor (Obesity factor).  
 Name=LEP; Synonyms=OB;  
 Macaca mulatta (Rhesus macaque);  
 OC Mammalia; Buteraria; Craniata; Vertebrata; Buteleostomi;  
 Cercopithecinae; Macaca.  
 [1]\_TaxID=9544;

SEQUENCE FROM N.A.

TISSUE=Adipose tissue;  
 MEDLINE=96411743; Pubmed=8810296; DOI=10.1074/jbc.271.41.25327;  
 Hotta K.; Gustafsson T.A.; Ortmeyer H.K.; Bodkin N.L.; Nicollson M.A.;  
 Hansen B.C.;  
 RT Regulation of obese (ob) mRNA and plasma leptin levels in rhesus  
 monkeys. Effects of insulin, body weight, and non-insulin-dependent  
 diabetes mellitus.;  
 J. Biol. Chem. 271:25327-25331(1996).

-I- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.

-I- SUBCELLULAR LOCATION: Secreted (Probable).

-I- SIMILARITY: Belongs to the leptin family.

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CC DR A041360; BAA95481; 1; - .

CC DR PA1159; 1AX8 .

CC DR IPB009079; 4\_helix\_cytokine .

CC DR IPB000065; Leptin\_ .

CC DR PF02024; Leptin\_1. .

CC DR PR00495; LEPTRIN. .

CC DR PD005698; Leptin\_1. .

CC DR HSSP; AAC50730.1; - .

CC DR SIGNAL; 1AX8 .

CC DR InterPro; IPR009079; 4\_helix\_cytokine .

CC DR InterPro; IPR000655; Leptin\_. .

CC DR Pfam; PF02024; Leptin\_1. .

CC DR PRINTS; PR00495; LEPTRIN. .

CC DR Prodrom; PD005698; Leptin\_1. .

CC DR Obesity; Signal\_ .

CC DR SIGNAL; 1 .

CC DR CHAIN .

CC DR DISULFID .

CC DR SEQUENCE .

Query Match Score 639; DB 1; Length 167; Best Local Similarity 86.3%; Pred. No. 9e-51; Mismatches 11; Indels 0; Gaps 0; Matches 126; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIQVQDPTKTKITIVTRINDISHTQSYSSKOKVTGLDFIPGSHPTLSKNDQTLAV 60

DB 22 VPIRKVQDDPTKTKITIVTRINDISHTQSYSSKOKVTGLDFIPGHPVLSKNDQTLAI 81

QY 61 YQQLTSMPSRNVIQISNDLENLRLHVAFLSKSCHLPWASGLETLDSIGGVLLEASGYS 120

DB 82 YQQLTGPSPRNVIQISNDLENLRLHVAFLSKSCHLPWASGLETLDSIGGVLLEASLYS 141

Query Match Score 672; DB 1; Length 167; Best Local Similarity 91.3%; Pred. No. 8 4e-54; Mismatches 13; Conservative 8; Indels 0; Gaps 0;

QY 1 VPIQVQDPTKTKITIVTRINDISHTQSYSSKOKVTGLDFIPGSHPTLSKNDQTLAV 60

DB 22 VPIQVQDPTKTKITIVTRINDISHTQSYSSKOKVTGLDFIPGHPVTLSQMDQTLAI 81

QY 61 YQQLTSMPSRNVIQISNDLENLRLHVAFLSKSCHLPWASGLETLDSIGGVLLEASGYS 120

DB 82 YQQLNLNLSRNVIQISNDLENLRLHVAFLSKSCHLPWASGLETLDSIGGVLLEASLYS 141

RESULT 8

Q6FB8 PRELIMINARY; PRT; 146 AA.

Q6FB8 AC Q6FB8; PRELIMINARY; PRT; 146 AA.

Q6FB8 DT 05-JUL-2004 (TREMBLrel. 27, Created)

Q6FB8 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

Q6FB8 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Lepin (Fragment).

OS *Bubalus bubalis* (Domestic water buffalo).

OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Buteraria; Ruminantia; Cetartiodactyla; Bovidae;

OC Bovinae; Bubalinae.

[1]\_TaxID=89462;

RN RP SEQUENCE FROM N.A.

RC TISSUE=adipose tissue;

RA Rajendran S., Shukla D.C., Saravanan B.C.;

OB\_FELCA STANDARD; PRT; 167 AA.

OB\_FELCA ID OB\_FELCA STANDARD; PRT; 167 AA.

OB\_FELCA AC Q6FB8; PRELIMINARY; PRT; 146 AA.

OB\_FELCA DT 05-JUL-2004 (TREMBLrel. 27, Created)

OB\_FELCA DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

OB\_FELCA DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

OB\_FELCA DE Lepin precursor (Obesity factor).

OB\_FELCA DE Leptin precursor (Obesity factor).

OB\_FELCA GN Name=LEP; Synonyms=OB;

OB\_FELCA OS *Felis silvestris catus* (Cat).

Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.

DR AY42059; AY8862.1;

HSPP: P41159; 1AY8.

DR GO: GO:005576; C: extracellular; IEA.

DR GO: GO:000179; F: hormone activity; IEA.

DR GO: GO:0007165; B: signal transduction; IEA.

InterPro: IPR0909; 4 helix\_cytokine.

InterPro: IPR00005; Leptin.

PFam: PF02024; Leptin\_1.

PRINTS: PR00395; LEPTIN.

ProDom: PD005698; Leptin\_1.

NON\_TER [1]

FT CHAIN <1 146 leptin.

FT CHAIN 146 AA; 16069 MW;

SEQUENCE IA745EE0851BD8CA CRC64;

Query Match Score 628; DB 2; Length 146;

Best Local Similarity 87.0%; Pred. No. 7-85-50;

Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKLTIKTVRINDISHTQVSSQKVTKGIDFIGLHPLTSLMDQTLAV 60

Db 1 VPIRKVQDTTKLTIKTVRINDISHTQVSSQKVTKGIDFIGLHPLTSLMDQTLAV 60

Qy 61 YQQILTSMPSRNVIQISNDLENLRDLHLYTAFSKSCHLWASGLTELDLSGGTEASYS 120

Db 61 YQQILTSLSPSRNVIQISNDLENLRDLHLYTAFSKSCHLWASGLTELDLSGGTEASYS 120

Qy 121 TEVVALSRQLGSQDMLRQDLSPGC 146

Db 121 TEVVALSRQLGSQDMLRQDLSPGC 146

#### RESULT 9

OB\_BOVIN STANDARD PRT; 167 AA  
 ID OB\_BOVIN P5095; 097918; Q9t533; Q9t529;  
 AC P5095; 097918; Q9t533; Q9t529;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Leptin precursor (Obesity factor).  
 GN Name=LEP; Synonyms=OB, OBS;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 NCBI TaxID:9913;

RN [1]

SEQUENCE FROM N.A.

TISSUE=Liver; Briscoe S., Vuocolo A.;

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 22-167 FROM N.A.

RA Ji S.; Sparlock M.E.;

RA "Partial cloning of bovine obesity gene.";

RL Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE OF 22-167 FROM N.A.

RA Kawakita Y.; Abe H.; Miyashige T.;

RA Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A., AND VARIANT CYS-25 AND VAL-80;

RC STRAIN=JERSEY; MEDLINE=20063685; PubMed=10594237;

RA Konfortov B.A.; Licence V.E.; Miller J.R.;

RT "Resequencing of DNA from a diverse panel of cattle reveals a high

level of polymorphism in both intron and exon.";

RL Mamm. Genome 10:1142-1145(1999).

[5]

RP SEQUENCE FROM N.A., AND VARIANT CYS-25.

RA Lieffers S.C.;

RT "Genotype effects of bovine leptin mutations on pre- and postpartum

RT leptin concentrations"; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

RN [6]

RP SEQUENCE OF 46-145 FROM N.A.

RA Lien S.; Sundvold H.; Klingland H.; Vaage D.I.;

RA "Two novel polymorphisms in the bovine obesity gene (OBs)." ;

RL Anim. Genet. 28:245-245(1997).

RN [7]

RP SEQUENCE OF 60-146 FROM N.A.

RX MEDLINE=96269621; PubMed=1661738;

RA Pfister-Genskow M.A.; Hayes H.; Eggen A.; Bishop M.D.;

RT "Chromosomal localization of the bovine obesity (OBs) gene." ;

RL Mamm. Genome 7:398-399(1996).

RN [8]

RP SEQUENCE OF 1-48 FROM N.A.

RA Fitzsimmons C.J.; Schmutz S.M.;

RT "Exon two of the bovine obese, leptin, gene." ;

RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

CC [-] FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.

CC [-] SUBCELLULAR LOCATION: Secreted (Probable).

CC [-] SIMILARITY: Belongs to the Leptin family.

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CC DR EMBL: U43943; AA85906.1; -

DR EMBL: U50365; AA861244.1; -

DR EMBL: U65793; AA806579.1; -

DR EMBL: AB003143; BAA19750.1; -

DR EMBL: AJ132754; CAB64255.1; -

DR EMBL: AU236854; CAB38018.1; -

DR EMBL: AU512638; CAD54745.1; -

DR EMBL: AJ512639; CAD54745.1; JOINED.

DR EMBL: X11369; CAB17197.1; -

DR EMBL: X43833; AAC18762.1; -

DR EMBL: AF120500; AAC23567.1; -

DR HSSP; PA1159; 1A88.

DR InterPro: IPR009079; 4 helix\_cytokine.

DR InterPro: IPR000065; Leptin.

DR Pfam: PF02024; Leptin\_1.

DR PRINTS: PR00495; LEPTIN\_1.

DR ProdDom: PD005698; Leptin\_1.

KW Obesity; Polymorphism; Signal.

FT SIGNAL 1 21 Potential.

FT CHAIN 22 167 Leptin.

FT DISULFID 117 167 By similarity.

FT VARIANT 25 25 R > C.

FT VARIANT 80 80 A > V.

FT CONFLICT 25 25 R > Q (in Ref. 2).

FT CONFLICT 166 166 G > E (in Ref. 2).

SQ SEQUENCE 167 AA; 18716 MW; 94C666B3069E50B7 CRC64;

Query Match Score 628; DB 1; Length 167;

Best Local Similarity 87.0%; Pred. No. 9.3e-50; Mismatches 9; Indexes 0; Gaps 0;

Matches 127; Conservative 10; Mismatches 10; Indexes 0; Gaps 0;

CC DR 1 VPICQVODDTKLTIKTVRINDISHTQVSSQKVTKGIDFIGLHPLTSLMDQTLAV 60

DR 22 VPICRQDDDKTLLIKTVRINDISHTQVSSQKVTKGIDFIGLHPLTSLMDQTLAV 81

DR 61 YQQITSMPSRNVIQISNDLENLRDLHLYTAFSKSCHLWASGLTELDLSGGTEASYS 120

DR 82 YQQITSLPSRNVIQISNDLENLRDLHLYTAFSKSCHLWASGLTELDLSGGTEASYS 141

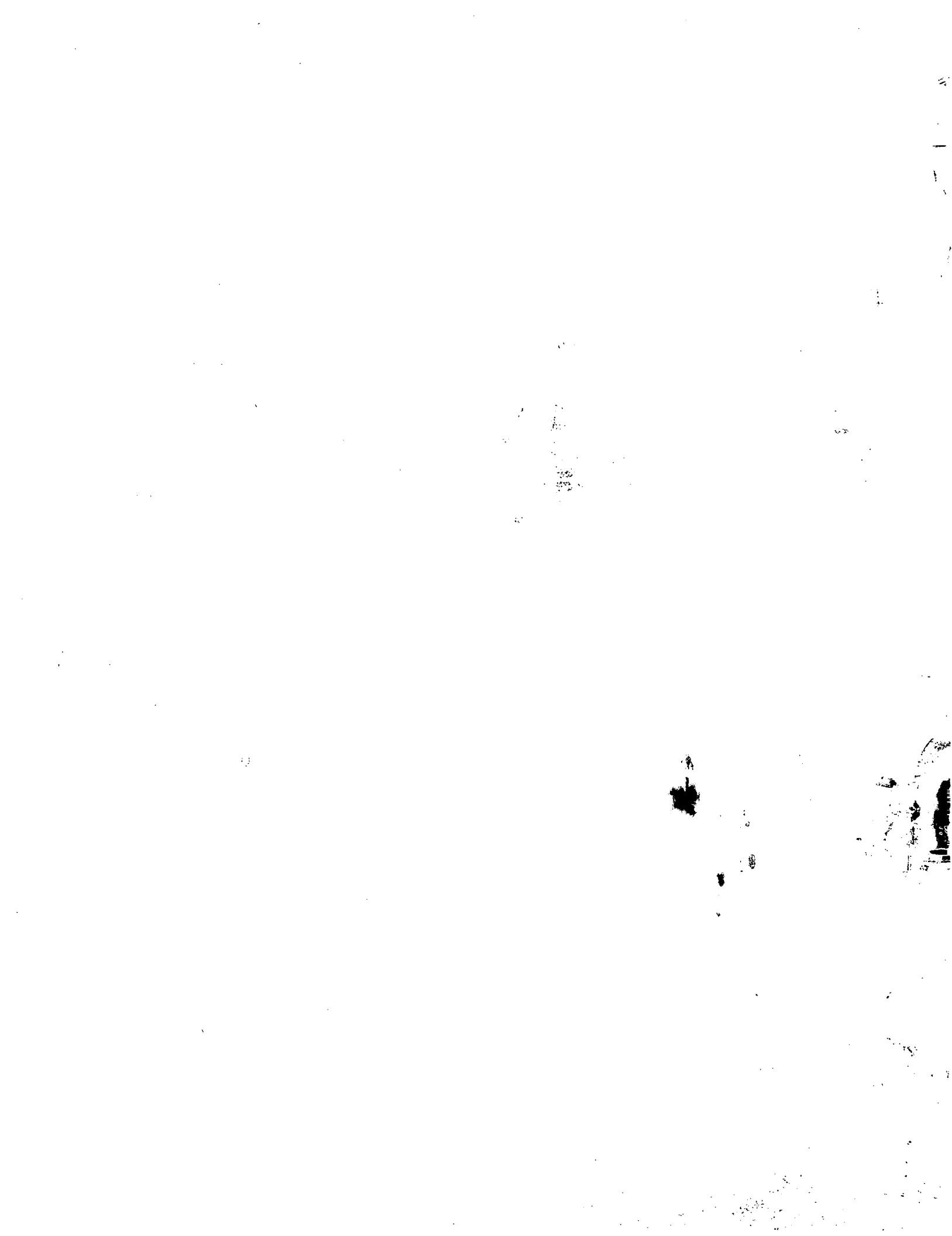
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY427959; AAR05862.1;  
 DR HSSP; P41059; IAX8;  
 DR GO; GO:000576; C: extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR007165; P: signal transduction; IEA.  
 DR Pfam; PRO00065; 4 helix.  
 DR PRINTS; PR00202; Leptin; 1.  
 DR PRODOM; PDD005698; Leptin.  
 PT NON\_TER  
 PT CHAIN  
 SQ SEQUENCE 146 AA; 146 leptin.  
 Query Match Score: 62.4; TDF2; Length: 146;  
 Best Local Similarity 85.3%; Pred. No.: 7.8e-50;  
 Matches 127; Conservative 10; MisMatches 9; Indels 0; Gaps 0;

Qy 1 VPIQKVDDTKLTIKTVTRINDIHSRQVSSESKRTGUDLPGVLLTISLKDPTLAV 60  
 Db 1 VPIRKVQDDTKLTIKTVTRINDIHSRQVSSESKRTGUDLPGVLLTISLKDPTLAV 60

Qy 61 YQQLITSMPSRNVIQISNDLENLRLHVLAFSKSCHLWASQLETLDSLGTVLEASGYS 120  
 Db 61 YQQLITSMPSRNVIQISNDLENLRLHVLAFSKSCHLWASQLETLDSLGTVLEASGYS 120

Qy 121 TEVVALSRQLQSGSDMMWQLDLSPGC 146  
 Db 121 TEVVALSRQLQSGSLQDMLRQLDLSPGC 146

RESULT 9  
 OB-BOVIN  
 ID OB BOVIN STANDARD  
 AC PS0595; Q97918; Q95133; O9msz9; PRT; 167 AA.  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DB Leptin precursor (Obesin factor).  
 GN Name=LEP; Synonyms=OB, OBS;  
 OS Bos taurus (Bovine).  
 OC Bovarioota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Bovinae; Bovidae; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 RN [1] -TAXID:9913;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Spurlock M.E.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2] SEQUENCE OF 22-167 FROM N.A.  
 RP Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 RC TISSUE=White adipose tissue.  
 RA Kawakita Y., Abe H., Miyashige T.;  
 RN [4] Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A., AND VARIANT CYS-25 AND VAL-80.  
 RC MEDLINE=20063685; PubMed=10594237;  
 RA Konfortov B.A.; Licence V.E. Miller J.R.;  
 RT "Resequencing of DNA from a diverse panel of cattle reveals a high  
 level of polymorphism in both intron and exon.";  
 RN [5] Genome 10:142-145 (1999).  
 RP SEQUENCE FROM N.A., AND VARIANT CYS-25.  
 RA Liefers S.C.;  
 RT "Genotype effects of bovine leptin mutations on pre- and postpartum



Qy 121 TEVVALSRQLGSQMLWQDLSPEC 146  
 Db 142 TEVVALSRQLGSQMLWQDLSPEC 167

**RESULT 10**

OB\_PIG ID OB\_PIG STANDARD; PRT; 167 AA.  
 AC Q27406; Q19095; Q5251;  
 AC DT 01-NOV-1997 (Rel. 35, Created)  
 AC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 AC DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Leptin precursor (obesity factor).  
 GN Name=LBP; Synonyms=OB, OBS;  
 OS Sus scrofa (Pig).  
 OC Batacota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=adipose tissue;  
 RA Louis C.F.;  
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ramsay T.G.; Yan X.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Landrace;  
 RA Robert C., Palin M.-F., Coulombe N., Roberge C., Silversides F.G.,  
 RA Benkel B.F., McKay R.M., Pelletier G.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Bidwell C.A., Ji S., Spurlock M.E.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Haishan;  
 RA Dai R., Li N., Hu X., Wu C.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA McNeel R.L., Mermann H.J.;  
 RT "adipose tissue regulatory transcript expression in lean versus obese  
 pigs.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=large white;  
 RA Soares M.A., Buciades R.F., Guimaraes S.E.F., Martins M.F.,  
 RA Lopes P.S.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE OF 15-110 FROM N.A.  
 RC TISSUE=White adipose tissue;  
 RX MEDLINE=9703921; PubMed=8836925;  
 RA Neuenschwander S., Rettenberger G., Meijerink E., Jorg H.,  
 RA Stranzinger G.;  
 RT "Partial characterization of porcine obesity gene (OBs) and its  
 localization to chromosome 18 by somatic cell hybrids.";  
 RL Anim. Genet. 27:275-278(1996).  
 CC -1- FUNCTION: May function as part of a signaling pathway that acts to  
 regulate the size of the body fat depot. An increase in the level  
 of leptin may act directly or indirectly on the CNS to inhibit food  
 intake and/or regulate energy expenditure as part of a homeostatic  
 mechanism to maintain constancy of the adipose mass.  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- SIMILARITY: Belongs to the leptin family.

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CC -----

CC DR EMBL; U63540; AAB05923.1;  
 CC DR EMBL; U63540; AAB03458.1;  
 CC DR EMBL; AF026976; AAB8274.1; -.  
 CC DR EMBL; U66254; AAB7308.1;  
 CC DR EMBL; AF052691; AAC06303.1; -.  
 CC DR EMBL; AF128856; AAC78147.1; -.  
 CC DR EMBL; AF477387; AAL84732.1; -.  
 CC DR EMBL; AF477386; AAL84732.1; JOINED.  
 CC DR EMBL; U63540; AAC8641.1; -.  
 CC DR EMBL; U63540; AAC8641.1; -.  
 CC DR HSSP; P41159; 1AX8;  
 CC DR InterPro; IPI00907; 4\_helix\_cytokine.  
 CC DR InterPro; IPI000055; Leptin.  
 CC PFam; PF02024; Leptin; 1.  
 CC DR PRINTS; PR000495; LEPTIN.  
 CC DR PRODOM; PD005698; Leptin; 1.  
 CC DR KW Obesity; Signal1.  
 CC FT SIGNAL; 1 21 Potential.  
 CC FT CHAIN 22 167 Leptin.  
 CC FT DISULFID 117 167 By similarity.  
 CC FT CONFLICT 21 22 AV -> GP (In Ref. 8).  
 CC FT CONFLICT 97 97 I -> L (In Ref. 8).  
 CC FT CONFLICT 122 122 A -> R (In Ref. 8).  
 CC SQ SEQUENCE 167 AA; 18661 MW; 27550E1E0B63814E CRC64;  
 CC  
 Query Match 85.2%; Pred. No. 1..1e-49;  
 Best Local Similarity 87.0%; Mismatches 9; Indels 0; Gaps 0;  
 Matches 127; Conservative 10; MisMatches 9;

QY 1 VPIQVQDDDTKTLTKITIVTRINDISHTOSVSSKVKVTGLDFIPGHPILTSKMDQTLAV 60  
 DB 22 VPINRQDDDTKTLTKITIVTRISDHMQSVSSKVKVTGLDFIPGHPVLTSKMDQTLAI 81

QY 61 YQQITSMPSRNVNQIISNDLENRLDHLVLAFSKSLPWASGLFTLDLSGGVFLASGYS 120  
 DB 82 YQQITSLPSRNVNQIISNDLENRLDHLVLAFFSKSLPWASGLFTLDLSGGVFLASLYS 141

QY 121 TEVVALSRQLGSQMLWQDLSPEC 146  
 DB 142 TEVVALSRQLGSQMLWQDLSPEC 167

**RESULT 11**

OB\_SHEEP ID OB\_SHEEP STANDARD; PRT; 146 AA.

AC Q2603; P79212;  
 AC DT 01-NOV-1997 (Rel. 35, Created)  
 AC DT 15-JUL-1998 (Rel. 36, Last sequence update)

DB Leptin (Obesity factor).  
 GN Name=LEP; Synonyms=OB;  
 OS Ovis aries (Sheep).  
 OC Bovariova; Chordata; Craniata; Vertebrata; Butelostomia;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Caprinae; Ovis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Adipose tissue;  
 RA Simmons J.M., Dyer C.J., Keisler D.H.;  
 RA Submitted (JAN-1997) to the EMBL/GenBank/DDBJ database.  
 RL [2]  
 RP SEQUENCE OF 9-125 FROM N.A.  
 RC TISSUE=Adipose tissue;  
 RA Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.;  
 RA Submitted (JAN-1997) to the EMBL/GenBank/DDBJ database.  
 RL [2]  
 RP SEQUENCE OF 9-125 FROM N.A.  
 RC TISSUE=Adipose tissue;  
 RA MEDLINE=98006799; PubMed=9347250; DOI=10.1016/S0139-7240(97)00028-3;  
 RA Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.;  
 RA "cDNA cloning and tissue-specific gene expression of ovine leptin,  
 CC NPY-Y1 receptor, and NPY-Y2 receptor.";

RL Domest. Anim. Endocrinol. 14:295-303(1997).  
 CC FUNCTION: May function as part of a signaling pathway that acts to  
 CC regulate the size of the body fat depot. An increase in the level  
 CC of LEP may act directly or indirectly on the CNS to inhibit food  
 CC intake and/or regulate energy expenditure as part of a homeostatic  
 CC mechanism to maintain constancy of the adipose mass.  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- SIMILARITY: Belongs to the leptin family.

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CC DR EMBL; U84247; AAB41786\_1; -;  
 CC DR EMBL; U62123; AAB51033\_1; -;  
 CC DR HSSP; P41159; 1AX8.  
 CC DR InterPro; IPR009079; 4 helix cytokine.  
 CC DR InterPro; IPR000065; Leptin.  
 CC DR Pfam; PF02024; Leptin\_1.  
 CC DR ProDom; PD005638; Leptin\_1.  
 CC KW Obesity.

DISU2ID 96 146 By similarity.  
 FT CONFLICT 65 65 L -> H (in Ref. 2);  
 FT CONFLICT 92 92 A -> G (in Ref. 2);  
 FT CONFLICT 124 124 V -> L (in Ref. 2);  
 SQ SEQUENCE 146 AA; 16053 MW; 19D5AC53240982CA CRC64;

Query Match Score 624; DB 1; Length 146;  
 Best Local Similarity 87.0%; Pred. No. 1.e-49;  
 Matches 127; Conservative 9; N mismatches 10; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDKTKLTIKTVTRINDIHTQSYYSSKKVTKLDFIPGHPIITLSKMDQTLLAV 60  
 Db 1 VPIRKVQDDKTKLTIKTVTRINDIHTQSYYSSKKVTKLDFIPGHPIITLSKMDQTLLAV 60  
 Qy 61 YQQLTSMPSRNVIQISNDLENLRLHLYAFSKSCHLPPWASGLTELDGGVYLEASGYS 120  
 Db 61 YQQLASLSPSNVIQISNDLENLRLHLLAASKSCPLPVRALESLESLGGVYLEASLYS 120  
 Qy 121 TEVVALSRLOGSLQMLWQDLSPGC 146  
 Db 121 TEVVALSRLOGSLQMLWQDLSPGC 146

RESULT 12  
 OB\_MOUSE STANDARD; PRT; 167 AA.  
 ID OB\_MOUSE  
 AC P41160;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Leptin precursor (Obesity factor).  
 GN Name=Lept; Synonyms=Ob;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 OX [1]

RP SEQUENCE FROM N.A. MEDLINE=9507553; PubMed=798236; DOI=10.1101/372425A0;  
 RX Zhang Y, Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.; "Positional cloning of the mouse obese gene and its human homologue." Nature 372:425-432(1994). [2]  
 RP ERRATUM. Zhang Y, Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.; Nature 374:479-479(1995). [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RA Chehab F.P., Jim M.B.; Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of Lep may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.  
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -!- DISEASE: Defects in Lep are the cause of profound obesity and type II diabetes.  
 CC -!- SIMILARITY: Belongs to the leptin family.  
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CC DR EMBL; U18812; AAA61564\_1; -;  
 CC DR EMBL; U22421; AAA64213\_1; -;  
 CC DR PIR; S509863; LTMS.  
 CC DR HSSP; PA1159; 1AX8.  
 CC DR MGD; MG1:104663; Lep.  
 CC DR GO; GO:0008083; F.growth factor activity; IDA.  
 CC DR GO; GO:0005151; F-protein binding; IPL.  
 CC DR GO; GO:0008206; P:beta acid metabolism; IDA.  
 CC DR GO; GO:0045639; Positive regulation of myeloid blood cell d. . . ; IDA.  
 CC DR GO; GO:0030300; P:regulation of cholesterol absorption; IDA.  
 CC DR InterPro; IPR009079; 4 helix cytokine.  
 CC DR InterPro; IPR000065; Leptin.  
 CC DR Pfam; PF02024; Leptin\_1.  
 CC DR PRINTS; PR00495; DPPTIN.  
 CC DR Probem; PD005698; Leptin\_1.  
 CC DR PRODOM; PD0030300; P:regulation of cholesterol absorption; IDA.  
 CC DR SIGNAL; 1 21 Leptin.  
 CC DR InterPro; IPR009079; Leptin.  
 CC DR FT CHAIN; 22 167 By similarity.  
 CC DR FT VARIANT; 117 167 Missing (in 30% the clones).  
 CC DR FT SEQUENCE; 167 AA; 18708 MW; D6783R6C76FD7116 CRC44;

Query Match Score 84.1%; Best Local Similarity 84.9%; Pred. No. 6.2e-49; Matches 124; Conservative 13; N mismatches 9; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDKTKLTIKTVTRINDIHTQSYYSSKKVTKLDFIPGHPIITLSKMDQTLLAV 60  
 Db 22 VPIQKVQDDKTKLTIKTVTRINDIHTQSYYSSKKVTKLDFIPGHPIITLSKMDQTLLAV 81

Qy 61 YQQLTSMPSRNVIQISNDLENLRLHLYAFSKSCHLPPWASGLTELDGGVYLEASGYS 120  
 Db 82 YQQVALSPSNVIQISNDLENLRLHLLAASKSCPLPVRALESLESLGGVYLEASLYS 120

Qy 121 TEVVALSRLOGSLQMLWQDLSPGC 146  
 Db 121 TEVVALSRLOGSLQMLWQDLSPGC 146

RESULT 13  
 OB\_RAT STANDARD; PRT; 167 AA.  
 ID OB\_RAT  
 AC P50596;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Leptin precursor (Obesity factor).  
 GN Name=Lept; Synonyms=Ob;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX	NCBI_TaxID=10116;	Db	22 VPIHKVQDDTKLTIKTVRINDISHTQSVAQRVTGDLFIPGLHPTLSKMDQTLAV 81
SEQUENCE FROM N.A.			
RC	TISSUE=Testis;	Qy	61 YQQITMSMRSNTIQINSNPLENRDLETFASNS CHLFWASGLTLDLGGVNLASGS 120
RX	Medline=55386724; PubMed=7657834;	Db	82 YQQITSLPSQNTIQIAHDLLENRLHLAFLSKSCSFLPOTRGLQPKESLDGVLEASLYS 141
RA	Ogawa Y., Matsuzaki H., Isse N., Okazaki T., Mori K., Shigemoto M.,	Qy	121 TEVVALSRQGSLQDMFLNQDLSPGC 146
RA	Satoh N., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,	Db	142 TEVVALSRQGSLQDMFLNQDLSPGC 167
RA	Nakao K.;		
RT	"Molecular cloning of rat obese cDNA and augmented gene expression in genetically obese Zucker fatty (fa/fa) rats.";		
RL	J. Clin. Invest. 96:1647-1652(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley; TISSUE=Fat;	RESULT 14	
RX	Medline=9514114; PubMed=779258;	OB_CANFA	STANDARD;
RA	Funahashi T., Shimomura I., Hirakata H., Arai T., Takahashi M.,	ID	OB_CANFA
RA	Nakamura T., Nozaki S., Yamashita S., Takemura K., Tokunaga K.,	AC	002720; Q9TSG1;
RT	"Enhanced expression of rat obese (ob) gene in adipose tissues of ventromedial hypothalamus (VMH)-lesioned rats."	DT	15-JUL-1998 (Rel. 36, Created)
RL	Biochem. Biophys. Res. Commun. 211:469-475(1995).	DT	16-OCT-2001 (Rel. 40, Last sequence update)
RN	[3]	DT	25-OCT-2004 (Rel. 45, Last annotation update)
RP	SEQUENCE FROM N.A.	DE	Lepin precursor (Obesity Factor).
RC	STRAIN=Levo, Olet/F, and Zucker; TISSUE=Adipose tissue;	GN	Name=LSP; Synonyms=OB;
RX	Medline=95251225; PubMed=773988;	OS	Canis familiaris (Dog).
RA	Murakami T., Shima K.;	EuCarYota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
RA	"Cloning of rat obese cDNA and its expression in obese rats."	OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RL	Biochem. Biophys. Res. Commun. 209:944-952(1995).	NCBItaxID=9615;	
RN	[4]	RN	
RP	SEQUENCE OF 14-167 FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN=Sprague Dawley; TISSUE=Fat;	RC	TISSUE=White adipose tissue;
RA	Donohoe P.A., Sivitz W.I., Bailey H.L.;	RA	Iwase M., Sasaki N., Komagome R., Kimura K., Saito M.;
RL	Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.	RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC	-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.	CC	-!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By similarity).
CC	-!- SUBCELLULAR LOCATION: Secreted (Probable).	CC	-!- SUBCELLULAR LOCATION: Belongs to the leptin family.
CC	-!- SIMILARITY: Belongs to the leptin family.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
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CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	CC	-----
CC	-----	CC	-----
DR	D45862; BAA08296.1; -	DR	AB020986; BAA35129.1; -.
EMBL	ST0586; AAB31657.2; -	DR	U95642; AAB53654.1; -.
EMBL	D44653; BAA08529.1; -	DR	HSSP_P41159; IAX8.
PIR	PC4034; LTTR2.	DR	InterPro; IPR009079; 4_helix_cytokine.
DR	HSSP_P41159; IAX8.	DR	InterPro; IPR000063; Leptin.
DR	RGD; 3000; Lep.	DR	Pfam; PF02024; Leptin_1.
DR	InterPro; IPR009079; 4_helix_cytokine.	DR	PRINTS; PR00445; LEPTIN.
DR	DR	DR	ProDom; PD00598; Leptin; 1.
DR	InterPro; IPR000065; Leptin.	KW	Obesity; Signal.
DR	PF0024; Leptin_1.	FT	SIGNAL 1 21 Potential.
DR	PRINTS; PR00445; Leptin.	FT	CHAIN 22 167 Leptin.
DR	ProDom; PD00598; Leptin.	FT	DISULFID 117 167 By similarity.
DR	KW	FT	CONFFLICT 32 167 K -> T (in Ref. 2).
FT	Obesity; Signal.	FT	CONFFLICT 163 163 L -> V (in Ref. 4).
FT	SIGNAL 1 21 Potential.	SQ	SEQUENCE 167 AA; 18866 MW; 3B5B563Da42Ec84E CRC64;
FT	CHAIN 22 167	FT	DISULFID 117 167 By similarity.
FT	DISULFID 117 167	FT	CONFFLICT 148 148 N -> S (in Ref. 2).
FT	CONFFLICT 32 167	SQ	SEQUENCE 167 AA; 18864 MW; 9703CFBED2286A55 CRC64;
FT	KW	FT	DISULFID 117 167 By similarity.
FT	CONFFLICT 163 163	FT	CONFFLICT 148 148 N -> S (in Ref. 2).
FT	SEQUENCE 167 AA; 18866 MW; 3B5B563Da42Ec84E CRC64;	SQ	SEQUENCE 167 AA; 18864 MW; 9703CFBED2286A55 CRC64;
Query Match	82.2%; Score 605; DB 1; Length 167;	Query Match	81.0%; Score 596; DB 1; Length 167;
Best Local Similarity	83.6%; Pred. No. 1.2e-47;	Best Local Similarity	82.2%; Pred. No. 8.1e-47;
Matches 122; Conservative 13; Mismatches 11; Indels 0; Gaps 0;	Matches 120; Conservative 13; Mismatches 13; Indels 0; Gaps 0;		
1 VPIQKVQDDTKLTIKTVRINDISHTQSVAQRVTGDLFIPGLHPTLSKMDQTLAV 60	Qy		

Db 22 VPIRKVQDDTKLTIKTVARINDISHTQSVSSKQRVAGLDFIPGILQPVLSRMDQTLLAI 81  
 Qy 61 YQQILTSMPSRNVIQISNDLENLRLHLVLAFLSKSCHLFLASGLETLDSUGGVLLEASGTS 120  
 Db 82 YQQILNSLHSRNVQISNDLENLRLHLVLAFLSKSCLPFLRGLTFLFESLGGVLLEASLYS 141  
 Qy 121 TEVVALSRQGSQSLQMLWQIDLSPGC 146  
 Db 142 TEVVALNRQLAQALQMLRLDLSPGC 167

RESULT 15  
 OB\_CHICK ID OB CHICK STANDARD: PRT: 163 AA.  
 AC 042154;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Leptin precursor (Obesity factor).  
 GN Name=IEP; Synonyms=OB;  
 OS Gallus gallus (Chicken).  
 OC Metzava; Metzora; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Shaver; TISSUE=Adipose tissue, and Liver;  
 RX MEDLINE=98201619; PubMed=9524275; DOI=10.1016/S0378-1119(97)00670-7;  
 RA Taouis M., Chen J. W., Daviaud C., Dupont J., Derouet M., Simon J.;  
 RT "Cloning the chicken leptin gene." /  
 RL Gene 20:39-242 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Broiler; TISSUE=Liver;  
 RA Ashwell C.M., Czerwinski S.M., McMurtrey J.P.;  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.  
 CC -I- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -I- TISSUE SPECIFICITY: Not exclusively localized in adipose tissue but is also expressed in liver.  
 CC -I- SIMILARITY: Belongs to the leptin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; AF012727; AAC0368.1; -.  
 DR EMBL; AF082500; AAC32380.1; -.  
 DR HSSP; P41159; IAX8.  
 DR InterPro; IPR009079; 4 helix\_cytokine.  
 DR InterPro; IPR000065; Leptin.  
 DR Pfam; PF02024; Leptin; 1.  
 DR ProDom; PD005698; Leptin; 1.  
 KW Obesity; Signal.  
 FT SIGNAL 1 18 Potential.  
 FT CHAIN 19 163 Leptin.  
 FT DISULFID 113 163 By similarity.  
 SQ SEQUENCE 163 AA; 18183 MW; 9E578DB528B3.8FC CRC64;

Query Match 79.7%; Score 586.5; DB 1; Length 163;  
 Best Local Similarity 82.2%; Pred. No. 5.9e-46;

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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:53:33 ; Search time 32.5463 Seconds  
(without alignments)  
383.035 Million cell updates/sec

Title: US-10-049-182-4

Perfect score: 870

Sequence: 1 MWGTLCGFLWLPYLFVQ.....SRLQGSILQDMLWQLDLSPGC 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cggn2\_6/ptcdatal1/iaa/5A\_COMB.pep:\*

2: /cggn2\_6/ptcdatal1/iaa/5B\_COMB.pep:\*

3: /cggn2\_6/ptcdatal1/iaa/6A\_COMB.pep:\*

4: /cggn2\_6/ptcdatal1/iaa/6B\_COMB.pep:\*

5: /cggn2\_6/ptcdatal1/iaa/PCUTS\_COMB.pep:\*

6: /cggn2\_6/ptcdatal1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the core of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	167	2 US-08-540-242A-4	Sequence 4, Appli
2	870	100.0	167	2 US-08-347-563A-4	Sequence 4, Appli
3	870	100.0	167	2 US-09-003-081-5	Sequence 5, Appli
4	870	100.0	167	3 US-08-292-345B-4	Sequence 4, Appli
5	870	100.0	167	3 US-08-648-262.5	Sequence 5, Appli
6	870	100.0	167	3 US-08-263.5	Sequence 5, Appli
7	870	100.0	167	3 US-08-648-263.5	Sequence 4, Appli
8	870	100.0	167	3 US-08-488-21A-4	Sequence 4, Appli
9	870	100.0	167	3 US-08-488-20A-4	Sequence 4, Appli
10	870	100.0	167	3 US-08-488-22B-1	Sequence 1, Appli
11	870	100.0	167	3 US-08-689-908.7	Sequence 7, Appli
12	870	100.0	167	3 US-08-433-21A-4	Sequence 4, Appli
13	870	100.0	167	3 US-08-488-222A-4	Sequence 4, Appli
14	870	100.0	167	3 US-09-147-805.4	Sequence 4, Appli
15	870	100.0	167	4 US-08-433A-4	Sequence 4, Appli
16	870	100.0	167	4 US-08-488-225A-4	Sequence 4, Appli
17	870	100.0	167	4 US-09-204-730B-4	Sequence 4, Appli
18	870	100.0	167	4 US-09-316-393.4	Sequence 4, Appli
19	870	100.0	167	4 US-09-377-081.17	Sequence 17, Appli
20	870	100.0	167	4 US-09-686-642A-4	Sequence 4, Appli
21	870	100.0	167	4 PCT-US96-01471-4	Sequence 4, Appli
22	870	100.0	397	4 US-08-775-066.2	Sequence 2, Appli
23	854.5	98.2	166	2 US-08-347-563A-6	Sequence 6, Appli
24	854.5	98.2	166	3 US-08-292-345G-6	Sequence 6, Appli
25	854.5	98.2	166	3 US-08-488-942A-6	Sequence 6, Appli
26	854.5	98.2	166	3 US-08-488-21A-6	Sequence 6, Appli
27	854.5	98.2	166	3 US-08-488-208A-6	Sequence 6, Appli

**ALIGMENTS**

RESULT 1  
US-08-540-242A-4  
; Sequence 4, Application US/08540242A  
; Patent No. 5627734

GENERAL INFORMATION:

APPLICANT: Weigle, David S.  
APPLICANT: Kuijper, Joseph W.  
APPLICANT: Forstrom, John W.  
APPLICANT: Lechner, Joyce M.  
TITLE OF INVENTION: APPETITE SUPPRESSION FACTOR AND RELATED METHODS  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADRESSEEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/540,242A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E.  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-01C5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 167 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-540-242A-4

Query Match 870 Score 100.0% Best Local Similarity 10.0% Matches 167 Conservatve 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 MWGTLCGFLWLPYLTVQAPIQVQIQQDDKTKLIIKTIIVTRINDISHTQSUSSSKQVYGL 60  
Db 1 MWGTLCGFLWLPYLTVQAPIQVQIQQDDKTKLIIKTIIVTRINDISHTQSUSSSKQVYGL 60

RESULT 3  
 US-09-003-081-5  
 ; Sequence 5 , Application US/09003081  
 ; Patent No. 5368779  
 / GENERAL INFORMATION:  
 / APPLICANT: Campfield, Arthur Dr.  
 / APPLICANT: Devos, Rene Dr.  
 / APPLICANT: Guisez, Yves Dr.  
 / TITLE OF INVENTION: Recombinant Obese (OB) Proteins  
 / NUMBER OF SEQUENCES: 8  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Hoffmann-La Roche, Inc.  
 / STREET: 340 Kingsland Street  
 / CITY: Nutley  
 / STATE: New Jersey  
 / COUNTRY: U.S.A.  
 / ZIP: 07110  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patent Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/003, 081  
 / FILING DATE:  
 / CLASSIFICATION: 514  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 08/435,777  
 / FILING DATE:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Picut, Catherine A.  
 / REGISTRATION NUMBER: 37419  
 / REFERENCE/DOCKET NUMBER: 9165  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (201) 235-2363  
 / TELEFAX: (201) 235-4387  
 / INFORMATION FOR SEQ ID NO: 5:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 167 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: not relevant  
 / TOPOLOGY: unknown  
 / MOLECULE TYPE: peptide  
 / HYPOTHETICAL: NO  
 / ANTI-SENSE: NO  
 / US-09-003-081-5

Query Match 1 MHWGLCGFLWLWPLFYQAVPQKVQDDTKTLIKTIVTRINDIHTQSVSQKVTGL 60  
 Best Local Similarity 100.0% Score 870; DB 2; Length 167;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 MHWGLCGFLWLWPLFYQAVPQKVQDDTKTLIKTIVTRINDIHTQSVSQKVTGL 60

Query Match 1 DFIPOLHPILTLSKMDQTLAVYQQLTSMPSRNVIQISNDLENLRLHVLAFSKSCHLP 120  
 Best Local Similarity 100.0% Score 870; DB 2; Length 167;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 DFIPOLHPILTLSKMDQTLAVYQQLTSMPSRNVIQISNDLENLRLHVLAFSKSCHLP 120

Query Match 1 MHWGLCGFLWLWPLFYQAVPQKVQDDTKTLIKTIVTRINDIHTQSVSQKVTGL 60  
 Best Local Similarity 100.0% Score 870; DB 2; Length 167;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 MHWGLCGFLWLWPLFYQAVPQKVQDDTKTLIKTIVTRINDIHTQSVSQKVTGL 60

Query Match 1 WASGLETLDSLGGVLEASGYSTEVALSRLQGSLOQDMWQLDLSPGC 167  
 Best Local Similarity 100.0% Score 870; DB 2; Length 167;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 WASGLETLDSLGGVLEASGYSTEVALSRLQGSLOQDMWQLDLSPGC 167

Query Match 1 MHWGLCGFLWLWPLFYQAVPQKVQDDTKTLIKTIVTRINDIHTQSVSQKVTGL 60  
 Best Local Similarity 100.0% Score 870; DB 2; Length 167;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 MHWGLCGFLWLWPLFYQAVPQKVQDDTKTLIKTIVTRINDIHTQSVSQKVTGL 60

RESULT 4  
 US-08-292-345B-4  
 ; Sequence 4 , Application US/08292345B  
 ; Patent No. 6001968  
 / GENERAL INFORMATION:  
 / APPLICANT: THE ROCKEFELLER UNIVERSITY  
 / TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF  
 / NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/292,345B  
 FILING DATE: August 17, 1994  
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE DOCKET NUMBER: 600-1-087

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEX: 13521  
 INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 167 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: Human Ob protein  
 ORIGINAL SOURCE: Human

US-08-292-345B-4

Query Match 100.0%; Score 870; DB 3; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-88;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MWGTLQGFLWMPYLFWQAVPIQVQDQTTLKTVTRINDISHTQSYYSKQXVGL 60

Qy 61 DFTPGLHPILTLSKMDQTLAVQQIITSMPSRNVIQISNDLNRLHVLAFSKSCHLP 120

Db 61 DFTPGLHPILTLSKMDQTLAVQQIITSMPSRNVIQISNDLNRLHVLAFSKSCHLP 120

Qy 121 WASGLETDLSLGCVLEASGYSTEVVALSRLOGSLQDMWQLDLSPGC 167

Db 121 WASGLETDLSLGCVLEASGYSTEVVALSRLOGSLQDMWQLDLSPGC 167

RESULT 6  
 US-08-648-263-5

Sequence 5, Application US/08648263

Patent No. 6025325

GENERAL INFORMATION:  
 APPLICANT: Campfield, Arthur  
 ATTORNEY: Devos, Rene  
 APPLICANT: Guisez, Yves  
 TITLE OF INVENTION: RECOMBINANT OBES E (OB) PROTEINS  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hoffmann-La Roche Inc.  
 STREET: 340 Kingsland Street  
 CITY: Nutley  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07110

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/648,263  
 FILING DATE: 15-MAY-1996  
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/484,629  
 FILING DATE: 07-JUN-1995  
 PRIORITY NUMBER: US 08/435,777

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

NAME: Kreisler, Lewis J  
 REGISTRATION NUMBER: 38522  
 REFERENCE DOCKET NUMBER: RAN 4105/175-002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 235-4363  
 TELEFAX: (201) 235-4387  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 167 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-648-263-5

Query Match 100.0%; Score 870; DB 3; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-88; Indels 0; Gaps 0;  
 Matches 167; Conservative 0; Mismatches 0; Gaps 0;

Qy	1 MWGTLICGFELWLPFLFYQAVPIKVQDDDTKLTKIVTRINDI	Qy	1 MWGTLICGFELWLPFLFYQAVPIKVQDDDTKLTKIVTRINDI
Db	1 MWGTLICGFELWLPFLFYQAVPIKVQDDDTKLTKIVTRINDI	Db	1 MWGTLICGFELWLPFLFYQAVPIKVQDDDTKLTKIVTRINDI
Qy	61 DFIPGLHPILTSKMDOTLAVYQQLTSMPSRNVIQISNDLENRLHLVLAFTSKCHLP 120	Qy	61 DFIPGLHPILTSKMDOTLAVYQQLTSMPSRNVIQISNDLENRLHLVLAFTSKCHLP 120
Db	61 DFIPGLHPILTSKMDOTLAVYQQLTSMPSRNVIQISNDLENRLHLVLAFTSKCHLP 120	Db	61 DFIPGLHPILTSKMDOTLAVYQQLTSMPSRNVIQISNDLENRLHLVLAFTSKCHLP 120
Qy	121 WASGLELTDLSGGVLEASGYSTEVALSRQLGSQMLWQDLSPGC 167	Qy	121 WASGLELTDLSGGVLEASGYSTEVALSRQLGSQMLWQDLSPGC 167
Db	121 WASGLELTDLSGGVLEASGYSTEVALSRQLGSQMLWQDLSPGC 167	Db	121 WASGLELTDLSGGVLEASGYSTEVALSRQLGSQMLWQDLSPGC 167

## RESULT 7

US-08-485-242A-4  
 Sequence 4, Application US/08485942A  
 / Patent No. 6048837  
 / GENERAL INFORMATION:  
 / APPLICANT: JEFFREY M. FRIEDMAN, YIXING ZHANG, RICARDO PROENCA,  
 / APPLICANT: MARGHERITA MAFFEI, JEFFREY HALARS, KETAN GAJIWALA, AND STEPHEN K. BURLE  
 / TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS  
 / TITLE OF INVENTION: AMENDED)  
 / NUMBER OF SEQUENCES: 99  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Klauber & Jackson  
 / STREET: 411 Hackensack Avenue  
 / CITY: Hackensack  
 / STATE: New Jersey  
 / COUNTRY: USA  
 / ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/485,942A  
 FILING DATE: JUNE 7, 1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/438,431  
 FILING DATE: May 10, 1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/347,563  
 FILING DATE: NO. 6048837ember 30, 1994  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/292,345  
 FILING DATE: August 17, 1994  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:

## RESULT 8

US-08-488-214A-4  
 Sequence 4, Application US/08488214A  
 / Patent No. 6124439  
 / GENERAL INFORMATION:  
 / APPLICANT: JEFFREY M. FRIEDMAN, YIXING ZHANG, RICARDO PROENCA,  
 / APPLICANT: MARGHERITA MAFFEI, JEFFREY HALARS, KETAN GAJIWALA, AND STEPHEN K. BURLE  
 / TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING  
 / TITLE OF INVENTION: (AS AMENDED)  
 / NUMBER OF SEQUENCES: 99  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Klauber & Jackson  
 / STREET: 411 Hackensack Avenue  
 / CITY: Hackensack  
 / STATE: New Jersey  
 / COUNTRY: USA  
 / ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/488,214A  
 FILING DATE: JUNE 7, 1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/438,431  
 FILING DATE: May 10, 1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/347,563  
 FILING DATE: NO. 6124439ember 30, 1994  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/292,345  
 FILING DATE: August 17, 1994  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,712  
 REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEX: 201 343-1684  
 TELEX: 133321  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 167 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: Human ob polypeptide  
 ORIGINAL SOURCE: Human  
 US-08-488-214A-4

Query Match 100.0%; Score 870; DB 3; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-88;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLICGFMLWPLFLYQVPIQRVQDDTKLTIKTTIVRINDIISHTQSYSSKQKVTRGL 60  
 Db 1 MHWGTLICGFMLWPLFLYQVPIQRVQDDTKLTIKTTIVRINDIISHTQSYSSKQKVTRGL 60  
 Qy 61 DFIPLGHHPILTSKMDQTLLAVYQQILTSMPSRNVIQISNDLENRLDLLVLAFSKSCHLP 120  
 Db 61 DFIPLGHHPILTSKMDQTLLAVYQQILTSMPSRNVIQISNDLENRLDLLVLAFSKSCHLP 120  
 Qy 61 WASGLETLDSLGGVLEASGYSTEVALSRQLGSQDMLWQDLSSFC 167  
 Db 61 WASGLETLDSLGGVLEASGYSTEVALSRQLGSQDMLWQDLSSFC 167  
 Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRQLGSQDMLWQDLSSFC 167  
 Db 121 WASGLETLDSLGGVLEASGYSTEVALSRQLGSQDMLWQDLSSFC 167

RESULT 9  
 US-08-488-208A-4  
 Sequence 4, Application US/08488208A  
 Patent No. 6124448

GENERAL INFORMATION:  
 APPLICANT: THE ROCKEFELLER UNIVERSITY  
 TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING  
 TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC  
 TITLE OF INVENTION: USES THEREOF  
 NUMBER OF SEQUENCES: 98  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent'n Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/488,208A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/485,943  
 FILING DATE: June 7, 1995  
 FILING DATE: 08/438,431  
 FILING DATE: MAY 10, 1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/347,563  
 FILING DATE: NO. 6124448ember 30, 1994  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/292,345  
 FILING DATE: August 17, 1994

CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-087 CIP21  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEX: 201 343-1684  
 TELEX: 133321  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 167 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: Human ob polypeptide  
 ORIGINAL SOURCE: Human  
 US-08-488-208A-4

Query Match 100.0%; Score 870; DB 3; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-88;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLICGFMLWPLFLYQVPIQRVQDDTKLTIKTTIVRINDIISHTQSYSSKQKVTRGL 60  
 Db 1 MHWGTLICGFMLWPLFLYQVPIQRVQDDTKLTIKTTIVRINDIISHTQSYSSKQKVTRGL 60  
 Qy 61 DFIPLGHHPILTSKMDQTLLAVYQQILTSMPSRNVIQISNDLENRLDLLVLAFSKSCHLP 120  
 Db 61 DFIPLGHHPILTSKMDQTLLAVYQQILTSMPSRNVIQISNDLENRLDLLVLAFSKSCHLP 120  
 Qy 61 WASGLETLDSLGGVLEASGYSTEVALSRQLGSQDMLWQDLSSFC 167  
 Db 61 WASGLETLDSLGGVLEASGYSTEVALSRQLGSQDMLWQDLSSFC 167

RESULT 10  
 US-08-759-628-1  
 Sequence 1, Application US/08759628  
 Patent No. 6225416

GENERAL INFORMATION:  
 APPLICANT: Altmann, Scott W.  
 APPLICANT: Rock, Fernando L.  
 APPLICANT: Bazan, J. Fernando  
 APPLICANT: Kasclein, Robert A.  
 TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent'n Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/759,628  
 FILING DATE: 05-DEC-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/008,574  
 FILING DATE: 06-DEC-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0552Q  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEXFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 167 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-759-638-1

Query Match 100.0%; Score 870; DB 3; Length 167;

Best Local Similarity 100.0%; Pred. No. 9.3e-88; Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1.2

Sequence 7, Application US/08688908

Patent No. 6297027

GENERAL INFORMATION:

APPLICANT: Spurlock, Michael E.

TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID

NUMBER OF SEQUENCES: 8

TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USES THEREOF

CORRESPONDENCE ADDRESS:

ADDRESSEE: WHITE HIRSCHBECK DUDEK S.C.

STREET: Suite 2100 111 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: USA

ZIP: 53202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/688,908

FILING DATE: 31-JUL-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Plotzcher, Gary R.

REGISTRATION NUMBER: 27,830

REFERENCE/DOCKET NUMBER: PM-8808

TELECOMMUNICATION INFORMATION:

TELEPHONE: 414-773-2100

TELEFAX: 414-223-5000

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 167 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-688-908-7

Query Match 100.0%; Score 870; DB 3; Length 167;

Best Local Similarity 100.0%; Pred. No. 9.3e-88; Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 870; DB 3; Length 167;

Best Local Similarity 100.0%; Pred. No. 9.3e-88; Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	MHWGTLCGFLMLWPLYVQAVPIQVQDDTTKTLIKTIVTRINDISHTQSSTSKQKVTLGL 60
Qy	61	DFPGLHPILTLSKMDQTLLAVYQQQLTSMPSRNVQISNDLLENLRLHVLAFSKSCHLP 120
Db	61	DFPGLHPILTLSKMDQTLLAVYQQQLTSMPSRNVQISNDLLENLRLHVLAFSKSCHLP 120
Qy	121	WASGLETLDSLGGVLEASGYCSTEVVVALSRQGSQIQLDMLWQDLSQPC 167
Db	121	WASGLETLDSLGGVLEASGYCSTEVVVALSRQGSQIQLDMLWQDLSQPC 167

RESULT 1.2

Sequence 4, Application US/08483211A

Patent No. 6309853

GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY

TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,211A

APPLICATION NUMBER: US/08/483,211A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/485,943

APPLICATION NUMBER: 08/347,563

APPLICATION NUMBER: 08/348,431

APPLICATION NUMBER: 08/438,431

FILING DATE: June 7, 1995

FILING DATE: May 10, 1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/09853ember 30, 1994

APPLICATION NUMBER: 08/292,345

APPLICATION NUMBER: 08/17, 1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 167 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: Protein

ORIGINAL SOURCE: Human ob polypeptide

US-08-483-211A-4

Query Match 100.0%; Score 870; DB 3; Length 167;

Best Local Similarity 100.0%; Pred. No. 9.3e-88; Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEWGTLCGLWNPYLFFQAVPIQRVQDDTKTLIKTVTRINDISHTQSYYSSKOKVTGL 60  
 Db 1 MEWGTLCGLWNPYLFFQAVPIQRVQDDTKTLIKTVTRINDISHTQSYYSSKOKVTGL 60

Qy 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLLENRLHVLAFSKSCHLP 120  
 Db 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLLENRLHVLAFSKSCHLP 120

Qy 121 WASGLELTDLSGGVLEASGYSTEVVALSRQLGSLODMLWQDLSPGC 167  
 Db 121 WASGLELTDLSGGVLEASGYSTEVVALSRQLGSLODMLWQDLSPGC 167

RESULT 13  
 US-08-488-223A-4 Application US/08488223A

GENERAL INFORMATION:  
 APPLICANT: THE ROCKEFELLER UNIVERSITY  
 TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THE NUMBER OF SEQUENCES: 98  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.1, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/488,223A  
 FILING DATE: 07-Jun-1995  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/485,943  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: 08/347,563  
 FILING DATE: NO. 1350730ember 30, 1994  
 APPLICATION NUMBER: 08/292,345  
 FILING DATE: August 17, 1994

ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Eng., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEX: 133321

INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 167 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: Human ob polypeptide  
 ORIGINAL SOURCE:  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

RESULT 14  
 US-09-147-805-4  
 Sequence 4, Application US/09147805  
 Patent No. 6399745  
 GENERAL INFORMATION:  
 APPLICANT: ERTL, Johann PREIBISCH, Gerald  
 MUELLER, Guenter  
 TITLE OF INVENTION: USE OF LEPTIN ANTAGONISTS FOR TREATING INSULIN RESISTANCE IN TYPE II DIABETES  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FOLEY & LARDNER  
 STREET: 3000 K Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.10  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/147,805  
 FILING DATE: 14-Apr-1999  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/EP97/05535  
 FILING DATE: 15-SEP-1997  
 APPLICATION NUMBER: DE 196 38 487.7  
 FILING DATE: 20-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Granados, Patricia D.  
 REGISTRATION NUMBER: 33,983  
 REFERENCE/DOCKET NUMBER: 026083/0200  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEFAX: (202) 672-5399  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 167 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-09-147-805-4

Query Match 100.0%; Score 870; DB 3; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-88; Indels 0; Gaps 0;  
 Matches 167; Conservative 0; MisMatches 0;

Qy 1 MHWGTLCGLWNPYLFFQAVPIQRVQDDTKTLIKTVTRINDISHTQSYYSSKOKVTGL 60  
 Db 1 MHWGTLCGLWNPYLFFQAVPIQRVQDDTKTLIKTVTRINDISHTQSYYSSKOKVTGL 60

Qy 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLLENRLHVLAFSKSCHLP 120  
 Db 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLLENRLHVLAFSKSCHLP 120

Qy 121 WASGLELTDLSGGVLEASGYSTEVVALSRQLGSLODMLWQDLSPGC 167  
 Db 121 WASGLELTDLSGGVLEASGYSTEVVALSRQLGSLODMLWQDLSPGC 167

Qy 121 WASGLELTDLSGGVLEASGYSTEVVALSRQLGSLODMLWQDLSPGC 167  
 Db 121 WASGLELTDLSGGVLEASGYSTEVVALSRQLGSLODMLWQDLSPGC 167

RESULT 15  
US-08-438-431A-4

Sequence 4, Application US/08438431A  
Patent No. 6429290

GENERAL INFORMATION:

APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MARFELI, TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR NUMBER OF SEQUENCES: 99

CORRESPONDENCE ADDRESS:  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.125

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438, 431A  
FILING DATE: May 10, 1995  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/347,563  
FILING DATE: NO. 6429290ember 30, 1994  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/292,345  
FILING DATE: August 17, 1994  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Jackson, Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-087 CIP1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 167 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
DESCRIPTION: Human ob polypeptide  
ORIGINAL SOURCE: Human  
US-08-438-431A-4

Query Match 100.0%; Score 870; DB 4; Length 167;  
Best Local Similarity 100.0%; Pred. No. 9 3e-88;  
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTICGFLMWPLFYAVPIKQVDDTKLTKTYTRINDISHTQSSTSKVTCI 60  
Db 1 MHWGTICGFLMWPLFYAVPIKQVDDTKLTKTYTRINDISHTQSSTSKVTCI 60

Qy 61 DFIPGHHPITLSKMDQTLLAVYQQILTMSRSRNYIQISNDLENRLHLVLAFSKSCHLP 120  
Db 61 DFIPGHHPITLSKMDQTLLAVYQQILTMSRSRNYIQISNDLENRLHLVLAFSKSCHLP 120

Qy 121 WASGLETLDSLGGLVEASGSTEVVALSRLQGSLODMNLQDMLNQLDISPGC 167  
Db 121 WASGLETLDSLGGLVEASGSTEVVALSRLQGSLODMNLQDMLNQLDISPGC 167

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OM protein - protein search, using sw model

Run on: March 12, 2005, 05:03:46 ; Search time 93.9042 Seconds  
(without alignments)

Scoring table: BLOSUM62

Title: US-10-049-182-4

Perfect score: 870

Sequence: 1 MWGTLGFLWLWPLYFVQ. .... SRLQGSIQDMLWQLDSLSPGC 167

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA:  
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 2: /cggn\_6/picodata/1/pubpa/US07\_PCTUS\_PUBCOMB.pep:  
 3: /cggn\_6/picodata/1/pubpa/US06\_NEWPUB.pep:  
 4: /cggn\_6/picodata/1/pubpa/US07\_NEWPUB.pep:  
 5: /cggn\_6/picodata/1/pubpa/US07\_PUBCOMB.pep:  
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 9: /cggn\_6/picodata/1/pubpa/US09A\_PUBCOMB.pep:  
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 18: /cggn\_6/picodata/1/pubpa/US11\_NEWPUB.pep:  
 19: /cggn\_6/picodata/1/pubpa/US60\_NEWPUB.pep:  
 20: /cggn\_6/picodata/1/pubpa/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	870	100.0	167	9 US-09-736-084-4	Sequence 4, Appli
2	870	100.0	167	9 US-09-736-084-4	Sequence 5, Appli
3	870	100.0	167	9 US-09-736-084-4	Sequence 6, Appli
4	870	100.0	167	9 US-09-736-084-4	Sequence 7, Appli
5	870	100.0	167	10 US-09-736-084-4	Sequence 8, Appli
6	870	100.0	167	15 US-10-440-464-67	Sequence 9, Appli
7	870	100.0	167	15 US-10-440-464-67	Sequence 10, Appli
8	870	100.0	167	15 US-10-440-464-67	Sequence 11, Appli
9	870	100.0	167	15 US-10-440-464-67	Sequence 12, Appli
10	870	100.0	167	15 US-10-440-464-67	Sequence 13, Appli
11	870	100.0	167	8 US-08-779-457-47	Sequence 14, Appli
12	870	100.0	167	17 US-10-921-710-47	Sequence 15, Appli
13	870	100.0	167	9 US-09-859-361-7	Sequence 16, Appli

RESULT 1  
US-09-736-084-4

; Sequence 4, Application US/09736084

; Patent No. US20020107211A1

; GENERAL INFORMATION:

; APPLICANT: THE ROCKEFELLER UNIVERSITY

; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC

; NUMBER OF SEQUENCES: 98

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klausber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS; SOFTWARE: Patent In Release #1., Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/736,084

; FILING DATE: 13-Dec-2000

; CLASSIFICATION: &lt;Unknown&gt;

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/438,431

; FILING DATE: May 10, 1995

; APPLICATION NUMBER: 08/347,563

; FILING DATE: NO. US 2010/211Aember 30, 1994

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Eng., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

Page 2

Qy 61 DFTPGLHPILTLSKMDDQTAVYQQILTSMPSRNVIOSINDLENRLHLVLAFSKSCHLP 120  
 Db 61 DFTPGLHPILTLSKMDDQTAVYQQILTSMPSRNVIOSINDLENRLHLVLAFSKSCHLP 120

Qy 121 WASGLETLDSGGVLEASGSTEVWALSRLQGSIQDMWQLDLSPOC 167  
 Db 121 WASGLETLDSGGVLEASGSTEVWALSRLQGSIQDMWQLDLSPOC 167

RESULT 4  
 US-09-804-409A-11  
 ; Sequence 11, Application US/09804409A  
 ; Patent No. US20020155100A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIEFFER, TIMOTHY J.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN  
 ; TITLE OF INVENTION: EXPRESSION IN GUT  
 ; CURRENT APPLICATION NUMBER: 0299961027 8721  
 ; FILE REFERENCE: 0299961027 8721  
 ; CURRENT PILING DATE: 2001-03-12  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 11  
 ; LENGTH: 167  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-804-409A-11

Query Match 100.0%; Score 870; DB 10; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-84;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLCGFLWLMWPFLFYQAVPIKVQDDDTKTLIKTIVRINDISHTQSYYSSKKQKVTLG 60  
 Db 1 MHWGTLCGFLWLMWPFLFYQAVPIKVQDDDTKTLIKTIVRINDISHTQSYYSSKKQKVTLG 60

Qy 61 DFTPGLHPILTLSKMDDQTAVYQQILTSMPSRNVIOSINDLENRLHLVLAFSKSCHLP 120  
 Db 61 DFTPGLHPILTLSKMDDQTAVYQQILTSMPSRNVIOSINDLENRLHLVLAFSKSCHLP 120

Qy 1 MHWGTLCGFLWLMWPFLFYQAVPIKVQDDDTKTLIKTIVRINDISHTQSYYSSKKQKVTLG 60  
 Db 1 MHWGTLCGFLWLMWPFLFYQAVPIKVQDDDTKTLIKTIVRINDISHTQSYYSSKKQKVTLG 60

Qy 121 WASGLETLDSGGVLEASGSTEVWALSRLQGSIQDMWQLDLSPOC 167  
 Db 121 WASGLETLDSGGVLEASGSTEVWALSRLQGSIQDMWQLDLSPOC 167

RESULT 6  
 US-10-440-464-67  
 ; Sequence 67, Application US/10440464  
 ; Publication No. US20040018528A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DEPRIMO, SAMUEL  
 ; APPLICANT: O'FARRELL, ANNE-MARIE  
 ; APPLICANT: MURAMOTO, ALYSSA  
 ; APPLICANT: SMOJICH, BEVERLY  
 ; APPLICANT: MANNING, WILLIAM  
 ; APPLICANT: WALTER, SARAH  
 ; APPLICANT: CHERPINGTON, JULIE  
 ; APPLICANT: SCHILLING, JIM  
 ; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE  
 ; FILE REFERENCE: 038602/1592  
 ; CURRENT APPLICATION NUMBER: US/10/440,464  
 ; PRIOR APPLICATION NUMBER: 60/380,872  
 ; PRIOR FILING DATE: 2003-05-19  
 ; PRIOR APPLICATION NUMBER: 60/448,922  
 ; PRIOR FILING DATE: 2003-02-24  
 ; NUMBER OF SEQ ID NOS: 185  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 67  
 ; LENGTH: 167  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-440-464-67

Query Match 100.0%; Score 870; DB 15; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-84;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLCGFLWLMWPFLFYQAVPIKVQDDDTKTLIKTIVRINDISHTQSYYSSKKQKVTLG 60

Page 4

1 MHWGLCFLWMPYLFFQAVPIQVQDDETRKTIKTVTRINDISHTQSISKQRTGGL 60  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-698-510-17

61 DFIPGHHPILTSKMDQTLLAVYQQILTSMPSRVNVIQISNDLENRLDILHVLAFSKSCLP 120  
 ; Sequence 17, Application US/10458334-17  
 ; Publication No. US2004004933A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Grasso, Patricia G.  
 ; APPLICANT: Lee, Daniel W.  
 TITLE OF INVENTION: Leptin-Related Peptides  
 FILE REFERENCE: AMC-1 Leptin Peptides (19705-001)  
 CURRENT APPLICATION NUMBER: US/10/458,334  
 CURRENT FILING DATE: 2003-06-09  
 PRIOR APPLICATION NUMBER: US/09/377,081  
 PRIOR FILING DATE: 1999-08-19  
 PRIOR APPLICATION NUMBER: U.S.S.N. 60/097,457  
 PRIOR FILING DATE: 1998-08-21  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 17  
 LENGTH: 167  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-458-334-17

RESULT 7  
 US-10-458-334-17  
 ; Sequence 17, Application US/10458334-17  
 ; Publication No. US2004004933A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Grasso, Patricia G.  
 ; APPLICANT: Lee, Daniel W.  
 TITLE OF INVENTION: Leptin-Related Peptides  
 FILE REFERENCE: AMC-1 Leptin Peptides (19705-001)  
 CURRENT APPLICATION NUMBER: US/10/458,334  
 CURRENT FILING DATE: 2003-06-09  
 PRIOR APPLICATION NUMBER: US/09/377,081  
 PRIOR FILING DATE: 1999-08-19  
 PRIOR APPLICATION NUMBER: U.S.S.N. 60/097,457  
 PRIOR FILING DATE: 1998-08-21  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 17  
 LENGTH: 167  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-458-334-17

Query Match 100.0%; Score 870; DB 15; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 2.7-e-84;  
 Matches 167; Conservative 0; Indels 0; Gaps 0;

Qy 1 MHWGLCFLWMPYLFFQAVPIQVQDDETRKTIKTVTRINDISHTQSISKQRTGGL 60  
 ; Sequence 17, Application US/10458334-17  
 ; Publication No. US2004004933A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Grasso, Patricia G.  
 ; APPLICANT: Lee, Daniel W.  
 TITLE OF INVENTION: Leptin-Related Peptides  
 FILE REFERENCE: 19705-001CIP  
 CURRENT APPLICATION NUMBER: US/10/698,510  
 CURRENT FILING DATE: 2003-10-31  
 PRIOR APPLICATION NUMBER: US 60/422,723  
 PRIOR FILING DATE: 2002-10-31  
 PRIOR APPLICATION NUMBER: US 09/377,081  
 PRIOR FILING DATE: 1999-08-19  
 SOFTWARE: PatentIn version 3.2  
 LENGTH: 167  
 SEQ ID NO: 17

RESULT 8  
 US-10-698-510-17  
 ; Sequence 17, Application US/10458334-17  
 ; Publication No. US2004004933A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Grasso, Patricia G.  
 ; APPLICANT: Lee, Daniel W.  
 TITLE OF INVENTION: Leptin-Related Peptides  
 FILE REFERENCE: 19705-001CIP  
 CURRENT APPLICATION NUMBER: US/10/698,510  
 CURRENT FILING DATE: 2003-10-31  
 PRIOR APPLICATION NUMBER: US 60/422,723  
 PRIOR FILING DATE: 2002-10-31  
 PRIOR APPLICATION NUMBER: US 09/377,081  
 PRIOR FILING DATE: 1999-08-19  
 SOFTWARE: PatentIn version 3.2  
 LENGTH: 167  
 SEQ ID NO: 17

Query Match 100.0%; Score 870; DB 17; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 2.7-e-84;  
 Matches 167; Conservative 0; Indels 0; Gaps 0;

Qy 1 MHWGLCFLWMPYLFFQAVPIQVQDDETRKTIKTVTRINDISHTQSISKQRTGGL 60  
 ; Sequence 17, Application US/10458334-17  
 ; Publication No. US2004004933A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Grasso, Patricia G.  
 ; APPLICANT: Lee, Daniel W.  
 TITLE OF INVENTION: Leptin-Related Peptides  
 FILE REFERENCE: 19705-001CIP  
 CURRENT APPLICATION NUMBER: US/10/698,510  
 CURRENT FILING DATE: 2003-10-31  
 PRIOR APPLICATION NUMBER: US 60/422,723  
 PRIOR FILING DATE: 2002-10-31  
 PRIOR APPLICATION NUMBER: US 09/377,081  
 PRIOR FILING DATE: 1999-08-19  
 SOFTWARE: PatentIn version 3.2  
 LENGTH: 167  
 SEQ ID NO: 17

RESULT 9  
 US-09-859-361-2  
 ; Sequence 2, Application US/09859361  
 ; Patent No. US2003005811A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Browne, Michael  
 ; Chapman, Conrad  
 ; Clinkenbeard, Helen  
 ; Robinson, Jeffrey  
 TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSSEE: SmithKline Beecham Corporation  
 STREET: 709 Svedland Road  
 CITY: King of Prussia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19406  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/859,361  
 FILING DATE: 17-May-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/981,783  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Baumeister, Kirk  
 REGISTRATION NUMBER: 33,833  
 REFERENCE/DOCKET NUMBER: P31202  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-270-5096  
 TELEFAX: 610-270-5090  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 396 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-859-361-2

Query Match 100.0%; Score 870; DB 9; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 8.9-e-84;  
 Matches 167; Conservative 0; Indels 0; Gaps 0;

Qy 1 MHWGLTLCGFILWPLFYQAVPIQRVQDDTKLTIKTVTRINDISHTQSVSQKVTGL 60  
 Db 1 MHWGLTLCGFILWPLFYQAVPIQRVQDDTKLTIKTVTRINDISHTQSVSQKVTGL 60

Qy 61 DFIGLHPILTLSKMDQTLLAVYQQITSMPSRNVTOISNDLENLRDLHVLAFLSKSCHLP 120  
 Db 61 DFIGLHPILTLSKMDQTLLAVYQQITSMPSRNVTOISNDLENLRDLHVLAFLSKSCHLP 120

Qy 121 WASGLETLDSLGGLVLEASGYSTEVALSRQLGSLSQDMLWOLDLSPGC 167  
 Db 121 WASGLETLDSLGGLVLEASGYSTEVALSRQLGSLSQDMLWOLDLSPGC 167

RESULT 10  
 US -08-859-361-5  
 Sequence 5, Application US/09859361  
 Patent No. US20020058311A1  
 GENERAL INFORMATION:  
 APPLICANT: Browne, Michael  
 Chapman, Conrad  
 Clinkenbeard, Helen  
 Robinson, Jeffrey  
 TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin  
 Domain and Use  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SmithKline Beecham Corporation  
 STREET: 709 Swedeland Road  
 CITY: King of Prussia  
 STATE: PA  
 ZIP: 19406

COMPILER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/859,361  
 FILING DATE: 17-May-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/981,783  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Baumeister, Kirk  
 REGISTRATION NUMBER: 33,833  
 REFERENCE/DOCKET NUMBER: P31202  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-270-5096  
 TELEFAX: 610-270-5090  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 396 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-859-361-5

Query Match 100.0%; Score 870; DB 9; Length: 396;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-84; Indels 0; Gaps 0;

Matches 167; Conservative 0; Missmatches 0;

1 MHWGLTLCGFILWPLFYQAVPIQRVQDDTKLTIKTVTRINDISHTQSVSQKVTGL 60  
 1 MHWGLTLCGFILWPLFYQAVPIQRVQDDTKLTIKTVTRINDISHTQSVSQKVTGL 60

Qy 61 DFIGLHPILTLSKMDQTLLAVYQQITSMPSRNVTOISNDLENLRDLHVLAFLSKSCHLP 120  
 Db 61 DFIGLHPILTLSKMDQTLLAVYQQITSMPSRNVTOISNDLENLRDLHVLAFLSKSCHLP 120

Qy 121 WASGLETLDSLGGLVLEASGYSTEVALSRQLGSLSQDMLWOLDLSPGC 167  
 Db 121 WASGLETLDSLGGLVLEASGYSTEVALSRQLGSLSQDMLWOLDLSPGC 167

RESULT 12  
 US-10-921-710-47

Sequence 47, Application US/10921710  
 Publication No. US20050019325A1  
 GENERAL INFORMATION:  
 APPLICANT: Carter, Paul J.  
 APPLICANT: Chians, Nancy Y.  
 APPLICANT: Kim, Kyung Jin  
 APPLICANT: Matthews, William  
 TITLE OF INVENTION: METHODS FOR IDENTIFYING ANTIBODIES THAT DECREASE BODY WEIGHT, FAT-DEPOT WEIGHT OR FOOD INTAKE IN AN OBESIVE ANIMAL  
 FILE REFERENCE: GENENT-53CP-C1  
 CURRENT APPLICATION NUMBER: US/10/921,710  
 CURRENT FILING DATE: 2004-08-18  
 PRIOR APPLICATION NUMBER: 08/779457  
 PRIOR FILING DATE: 1997-01-07  
 PRIOR APPLICATION NUMBER: 60/064855  
 PRIOR FILING DATE: 1996-01-08  
 PRIOR APPLICATION NUMBER: 08/585605  
 PRIOR FILING DATE: 1996-01-08  
 PRIOR APPLICATION NUMBER: 08/667197  
 PRIOR FILING DATE: 1996-06-20  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 47  
 LENGTH: 397  
 TYPE: PR  
 ORGANISM: Homo sapiens  
 US-10-921-710-47

Query Match Score 870; DB 17; Length 397;  
 Best Local Similarity 100.0%; Pred. No. 8..9e-84;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWGTLUGFLMLWPFLYQAVPIQVQDPLKTKLKTIVTRINDISHTQSSKOKVTGL 60  
 Db 1 MWGTLUGFLMLWPFLYQAVPIQVQDPLKTKLKTIVTRINDISHTQSSKOKVTGL 60

Query Match Score 870; DB 9; Length 399;  
 Best Local Similarity 100.0%; Pred. No. 9e-84;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWGTLUGFLMLWPFLYQAVPIQVQDPLKTKLKTIVTRINDISHTQSSKOKVTGL 60  
 Db 1 MWGTLUGFLMLWPFLYQAVPIQVQDPLKTKLKTIVTRINDISHTQSSKOKVTGL 60

Qy 1 MWGTLUGFLMLWPFLYQAVPIQVQDPLKTKLKTIVTRINDISHTQSSKOKVTGL 60  
 Db 1 MWGTLUGFLMLWPFLYQAVPIQVQDPLKTKLKTIVTRINDISHTQSSKOKVTGL 60

Qy 61 DFIPGLHPPLTLSKMDQTLLAVYQQLTMSPSRNVNQIISNDLENRLDILVLAFSKSCHLP 120  
 Db 61 DFIPGLHPPLTLSKMDQTLLAVYQQLTMSPSRNVNQIISNDLENRLDILVLAFSKSCHLP 120

Qy 121 WASGLETLDSLGGVLEASGYSTEVVALSLQGSQLDMLWQDLSPGC 167  
 Db 121 WASGLETLDSLGGVLEASGYSTEVVALSLQGSQLDMLWQDLSPGC 167

RESULT 14  
 US-09-859-361-9  
 Sequence 9, Application US/09859361  
 Patent No. US20050058311A1  
 GENERAL INFORMATION:  
 APPLICANT: Browne, Michael  
 Chapman, Conrad  
 Clinkenbeard, Helen  
 Robinson, Jeffrey  
 TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SmithKline Beecham Corporation  
 STREET: 709 Swedeland Road  
 CITY: King of Prussia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19406  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/859,361  
 FILING DATE: 17-May-2001

Computer Readable Form:  
 Medium Type: Diskette  
 Computer: IBM Compatible  
 Operating System: DOS  
 Software: FastSEQ for Windows Version 2.0  
 Current Application Data:  
 Application Number: US/09/859,361  
 Filing Date: 17-May-2001

Classification: <Unknown>  
 Attorney/Agent Information:  
 Name: Baumeister, Kirk  
 Registration Number: 33,833  
 Reference/Docket Number: P31202

Classification: <Unknown>  
 Prior Application Data:  
 Application Number: 08/981,783  
 Filing Date: Unknown

Classification: <Unknown>  
 Attorney/Agent Information:  
 Name: Baumeister, Kirk  
 Registration Number: 33,833  
 Reference/Docket Number: P31202

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096

TELEFAX: 610-270-5090

INFORMATION FOR SEQ ID NO: 9:

## SEQUENCE CHARACTERISTICS:

LENGTH: 401 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-859-361-9

Query Match 100.0% Score 870; DB 9; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-84;  
 Mismatches 0; Indels 0; Gaps 0;

Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLICGFLWMPYLPIVQAVPIKVQDPTKLIKIVTRINDISHTQSVSQKVTVGL 60  
 Db 1 MHWGTLICGFLWMPYLPIVQAVPIKVQDPTKLIKIVTRINDISHTQSVSQKVTVGL 60

Qy 61 DFIPGHPLIPLTSKMDQTLAVYQQILTSMPSRNVQISNDLENLFDLHLTVAFSKSCHLP 120  
 Db 61 DFIPGHPLIPLTSKMDQTLAVYQQILTSMPSRNVQISNDLENLFDLHLTVAFSKSCHLP 119

Qy 121 WASGLETLDSLGGVLEASGSTEVVALSRQLGSLODMNLQDLSSGC 167  
 Db 121 WASGLETLDSLGGVLEASGSTEVVALSRQLGSLODMNLQDLSSGC 166

Qy 122 WASGLETLDSLGGVLEASGSTEVVALSRQLGSLODMNLQDLSSGC 167  
 Db 122 WASGLETLDSLGGVLEASGSTEVVALSRQLGSLODMNLQDLSSGC 167

RESULT 15

US-09-736-084-6

Sequence 6, Application US/09736084

Patent No. US2002010721A1

## GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY

TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

NUCLEOTIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC

## NUMBER OF SEQUENCES: 98

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber &amp; Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/736,084

FILING DATE: 13-D-C-2000

CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/438,431

FILING DATE: May 10, 1995

APPLICATION NUMBER: 08/347,563

FILING DATE: No. US2002010721A1ember 30, 1994

APPLICATION NUMBER: 08/29/,345

FILING DATE: August 17, 1994

## ATTORNEY/AGENT INFORMATION:

NAME: Jackson Bsq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

INFORMATION FOR SEQ ID NO: 6:

## SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: Human ob polypeptide lacking Gin at position  
 ORIGINAL SOURCE:  
 ORGANISM: Human  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-736-084-6

Query Match 98.2%; Score 854.5; DB 9; Length 166;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-82;  
 Matches 166; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MHWGTLICGFLWMPYLPIVQAVPIKVQDPTKLIKIVTRINDISHTQSVSQKVTVGL 60  
 Db 1 MHWGTLICGFLWMPYLPIVQAVPIKVQDPTKLIKIVTRINDISHTQSVSQKVTVGL 59

Qy 61 DFIPGHPLIPLTSKMDQTLAVYQQILTSMPSRNVQISNDLENLFDLHLTVAFSKSCHLP 120  
 Db 60 DFIPGHPLIPLTSKMDQTLAVYQQILTSMPSRNVQISNDLENLFDLHLTVAFSKSCHLP 119

Qy 121 WASGLETLDSLGGVLEASGSTEVVALSRQLGSLODMNLQDLSSGC 167  
 Db 120 WASGLETLDSLGGVLEASGSTEVVALSRQLGSLODMNLQDLSSGC 166

Search completed: March 12, 2005, 05:21:03  
 Job time : 94.9042 secs

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